

```
QY 665 -----LeuThrLeuGlnGlyLeuProGlu 672
Db 5221 TTTCTAATGCAATATATAGACTTTTTCACGCAATTAGATATAGTGGACACCA--- 5277
QY 673 GlyTyrSerTyrLeuVal-----LysGluThrAspSerGluGly 685
Db 5278 GGAGTTAATCTATCTTCGTAAATGTTCTTTTAAACGCCCAAACTCGGATTAAGTCAAA 5337
QY 686 TyrLysValLysValAsnSerGlnGluValAlaAsnAlaThrValSerLysThrGlyLe 705
Db 5338 CTGTCTACAAAGTCACTCGCAACACAGTCACC----- 5370
QY 706 ThrSerAspGluThrLeuAlaPheGluAsnAsnLysGluProValValProThrGlyVal 725
Db 5371 -----GAAAACTTCGTGGATGTCACAGGTGCCAAATTCACCTGCACCAACAGGCTTC 5421
QY 726 AspGln 727
Db 5422 ACCCAA 5427
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Search completed: August 19, 2003, 19:55:37  
Job time : 580 secs

Best Local Similarity:	20.20%	Mismatches:	301
Query Match:	3.52%	Indels:	214
DB:	10	Gaps:	39
US-09-494-297-2 (1-757) x US-09-070-927A-167 (1-19031)			
OY	5	ArgPheProAsnIlySLeuAsnThIleuAsnThrGlnArgValIleuSerGlyAsnSerIlyS	24
Db	3547	AAGTTTACTAATATTTTGTATCGTATTAATACATTGATGCGAAAGTAATAC-----	3600
OY	25	ArgPheThrValThIleuValGValPheIleuMetIlePheAlaIleuValThIleuMet	44
Db	3601	-----ATAGGTTATPAGACGTGTGACTACSSCAATGATTAATACCATGTG	3642
OY	45	ValGlnAlaIlySerThIlePheGlyLeuValGluSerSerThIleProAsnAlaIleAsnPro	64
Db	3643	ACCAACGCGCGTGCACGAAACCTGTGATGATCAAGTGCGCGCAAAATACGCGCA	3702
OY	65	AspSerSerSerGluTyrArgTyrGlyTyrGluSerTyrValArgGlnIlyProTyr	84
Db	3703	AGTAAATTTCACCCAA-----GCGAAACAAACGCGCATTAACAGATGACCTTAC	3750
OY	85	TyrIlyGlnPheArgValAlaIleAsnIleAspLeuArgValAsnIleuGluGlySerArgSerTyr	104
Db	3751	-----ACGTTC	3756
OY	105	GlnValTyrCysPheAsnIleuIlySAlaPheProIleuGlySerAspSer---SerVal	123
Db	3757	CACAAAGTGTTTT---TTACCGGAGACGCTACAAAGTGCGACGAATCTTACCGATTC	3813
OY	124	IlyIlySerTyrTyrIlyIlySlyAsnIlyIleSerThIlySlyPheGluAspTyrAlaMet--	142
Db	3814	AAAGCGTGGTCAAAAGG-----AAACCAAAACCGGACCTTGGCCACACACT	3861
OY	143	-----SerProArgIleThIleGlyAspGluIleuAsnGlnIlySleuArgAlaIleMet	159
Db	3862	AAACACCTACTCTTAAGTACGTATGATAC---AATGATGATTTGACGCGTGTAT	3918
OY	160	-----TyrAsnGlnIlyS---ProGlnAsnAlaAsn-----GlyIleMetGluGly	173
Db	3919	GAGGAGTTTTGAGGTTGACGAGCTGCGCTTGCAACAAATGATTTGGCTTTGTGAT---	3975
OY	174	IleuGluPheIleuAsnAlaIleArgValThIleGlnAlaValTyrTyrTyrSerAspAsn	193
Db	3976	---GAGCGACGAACAATTAATTGATGCGCGCCGACCAAGTGCGAGTAAATAT---	4026
OY	194	AlaProIleSerAsnProAspGluSerPheIlyAsnArgIleuSerGluSerIleuValSer	213
Db	4027	-----CTTACTTTAAATGAATAATATTAATAAAACAGTATGACGACGATTAATACGGGG	4080
OY	214	ThIleSerGlnIleuSerLeuMetArgGlnAlaIleuIlySglnIleuIleAspProAsnIleuAla	233
Db	4081	ACAGATACAGCGACACGT-----AAAACTTGTC	4110
OY	234	ThIlyMetProIlySglnValProAspAspPheGlnIleuSerIlePhe---GluSerGlu	252
Db	4111	-----GTGCTGTCACTATTTTGAACAATATGCGCTCAATAGCTTTTATGCGCGAGT	4164
OY	253	AspIlySglnAspIlySlyIlySglnIlyGlnIleuSerGlyGlyIleuValPro	272
Db	4165	GACATTACGTTTACATTGCCCAAAAGGTAACAATCAATATAT---	4209
OY	273	ThIlySProProThrProGlyAspProPheMetPro---ProAsnGlnProGlnIlyThr	291
Db	4210	ACCAAAATCAGATGCGCAAAACGCGACGCTTTCTCTTCTTAAATCTTAATATATGAT	4269
OY	292	SerValIleuIleArgIlyTyrAlaIleGlyAspTyrSerIlyIleuGluGlyAlaThr	311
Db	4270	CAAGTAGAATATGTCACATGCGCTGTGCACCACTATTAACAAGTTG-----	4314
OY	312	IleuGlnIleuThrGlyAspAsnValAsnSerPheGlnAlaArgValIleSerSerAspAsp	331
Db	4315	AAACAGCTGTGCGGCT-----CAACGTTTGGCTTTAAATGCT	4350

OY	332	lleglgluagnglllegluleusefaspolythrtyrtyrleuthrthgluleanserpro	351
OY	4351	TTAGCGGATCAACCTGAATTT-----TATACGAACCACTTATTTGGGCAACAG	4398
OY	352	AlaglytYserIleAlagIuProIlethrPheIysValGlualagIylsValtyrthr	371
Db	4399	TCTGGC-----ATCGATGACCCAGCACTAATTATATACAAATGAGTGGCCGTTTAC---	4449
OY	372	lIleIleaspglyIysGlnIlegluleansProasnIysGlnIleValGlulProtyrserVal	391
Db	4449	-----	4449
OY	392	GlualatyranaspphegluglupheserValleuthrthnglnasntyAlalysphe	411
Db	4449	-----	4449
OY	412	TyrtyralalysasnIysasnIyserserglnValtyrCysPheasnAlaspleu	431
Db	4450	TATATATTAGAAAACCGCAAGTACACGAGAACCTTGAGACACCAACGCGGCTAAATC	4509
OY	432	LysserProproasrsergluaspolyltyrthr---MetthrProaspphehrthr	450
Db	4510	ACACCGCCACAGCTTTCACCCAAAGTAAAAAACGGTATTACAAGCAC-----	4560
OY	451	glyIuValysTythrthnsllealagIyArgaspleuPheIysTythrValtyrPro	470
Db	4561	-----GCCATACCTTCAACAA	4578
OY	471	ArgaspphrasproasPthrPheuleuIyshtleIysIysValIleglulysgltyr	490
Db	4579	GCAGGCACTTACACAGACACTTACAAACAGCGGTAGACCTCAAGCTCAAGGTTGG	4638
OY	491	ArgIuIysglIyGlnAlleIleglutysergluIeuthrIuThrngIeulArqAlala	510
Db	4639	---TACAAAGGCAAGTCCATA---CTCAACACATTGACAACTACC-----AAAGCCCA	4688
OY	511	ThrIeuleuAlleIeTythrPheThrPheasrAlagluleu-----AspIysAspIys	528
Db	4687	AGTATATCAAGTACCTACGATGACAAATGATATTGTAATGCGTATGAAAGAAACAA	4748
OY	529	IeulysaspyrthIasglIyPheglIyAspMetasn-----Asper	541
Db	4747	GTTACACAGACGTGATCCATCAGTGTGATGGAACCTTTGCAATGAAAAAGCGGGCTTTC	4806
OY	542	ThrIeulavalAlalysIleleuValgluTyraIagIuasPserasnProProglIeul	561
Db	4807	ACACCGCGGTTAACTTTAGTGTGTAAGTACTATGGGCAAGTACAGGCTACTTAGA	4866
OY	562	Thraspleu---AspphePheIleProasnsnasnIysTyrglnIserIleuIleglythr	580
Db	4867	ACCGATTTATATGACGTGACCTCAAAAATATATGTAAATGGCAATATAGCGTAATTT	4928
OY	581	GlntrphtIasProglIuaspleu---ValaspleIleIeargmetglIuaspleuIysgluVal	599
Db	4927	AATATAGTGTACTATGCGCATTTGCCACAGAAATTATTGAAAAAATATAATATGACACACCA	4986
OY	600	IleProValIthrHIsasnleuthrIeulargIysThrValIthrGlyIeulAlaGlyAspArg	619
Db	4987	ATCAGTGTCCACACACAGATTCACGTTT---AATGTTGATTAATATGCCATGACACCA	5040
OY	620	ThryIyaspphehtIasPhegluIlegluleuIysasnIysGlnIleuIleuIeuser---	638
Db	5041	CAACTAAATATATGTTGACAGCATTAATTAACAGCTCAAACTAGCAATCTGAATCTC	5100
OY	639	---GlntrhValIysThraspleuIthrAsnleuglupheIysaspglyIysAla-----	655
Db	5101	TATGATATATGTACACGAACAATATAGCTCACTGTTTTCGACCCAAATATGACACACAGA	5160
OY	656	-----ThIleasnleuIyshtIasglIeuser-----	664
Db	5161	GAGGTGACCTTAAGTTCAGATTCCTTAACCTTAACTTGAATTTTGGATTCGATGACCACTAT	5220

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OY 368 LysValTyr-----Phtle-----IleaspGlyLysGlnIleGlu 379
DB 5713 TTTAAATATTTTCCCCACCTAATACACTTGATGAAACCTAGAACGACGATTTGAT 5772
OY 380 AsnProAsnLysGluIleValGluPro-----TyrSerValGluIleTyrAsnAsp 396
DB 5773 TTTACTGAAAAATTTATTTATGACGAAAAATTTATTTATTTGATGATTAATATAGAGA 5832
OY 397 PheGluGluPheSerValIleuThrThrGlnAsnTyrAlaLysPheTyrTyrAla----- 414
DB 5833 GCTGTAGATGGAAGAAATTACATGCTGGAATGCAC-----TATTTAGCCGAGAA 5883
OY 415 -----LysAsnLysAsnGlySerSerGlnValValTyrCysPheAsnAla 429
DB 5884 ACAGGTAAGCTTTTAAAGCTTAATCAATAAGGATTAATTAATTAATTAATTAATTAAT 5943
OY 430 Asp-----LeuLysSerProProAspSerGluAspGlyLysThrMetThrProAsp 447
DB 5944 GATGAGTATATGCAAAAAGATTTGTTGATTAATAATGATTAATAACACTATTTTGATGAT 6003
OY 448 PheThrThrGlyGluValLysTyrThrHisIleAlaGlyArg----- 461
DB 6004 TCTGTGTATGTAAGGTAGTTACACTGAAATAGATGCGACACTTCTACTTGTGCGAA 6063
OY 462 -----AspLeuPheLysTyrThrValLys 469
DB 6064 AACGGAAATGCAAAATAGGACTATTTAATACAGAAAGATGATTTAATAAT----- 6114
OY 470 ProArgAspThrAspProAspThrPheLeuLysHisIleLysValIleGluLysGly 489
DB 6115 -----TTTGCTCATCATATGAAAGATTTA----- 6138
OY 490 TyrArgGluLysGlyAlaIleGluTyrSerGlyLeuThrGluThrGlnLeuArgAla 509
DB 6139 GGAATGAAAGGAGGCAAAATCTCATTTCTGTATTAATTAATTAATTAATTAATAA--- 6195
OY 510 AlaThrGlnLeuAlaIleTyrTyrPheThrAspSerAlaGlu----- 523
DB 6196 -----ATTACTATTTTGATGATCTTACAGCTGCTACTTGATGGAGAA 6240
OY 524 -----LeuAspLysAspLysLeuLysAspTyrHisGly 534
DB 6241 GATTAGAGAGATGTTCAAAAGTATTATTGATGAAGATACAGACAGACATATATAGGT 6300
OY 535 PheGlyAspMetAsn-----AspSerThrLeuAlaValAla 546
DB 6301 TTGTCATTATTAATTAAGTGCATAATTTAATGATGATGAAATTTATGCAAGTTGCA 6360
OY 547 LysIleLeuValGlu----- 551
DB 6361 TTTCACACTATAAATGATAAAGCTTTCTACTCTGACTCTGGAATTTAGAAATCTGCA 6420
OY 552 -----TyrAlaGlnAspSerAsnProGlnLeuThr 562
DB 6421 GTACAAAACATAGATGACACATATTATTCTATATAGATGAATAGGTACTGTAATTTGCT 6480
OY 563 AspLeuAsp-----PhePheIleProAsnAsnAsn----- 572
DB 6481 GATTTGATATCTTCAGATGATATAAATTTTTCACCTGCTAAATACTGTAATATGATAT 6540
OY 573 -----LysTyrGlnSerLeu----- 577
DB 6541 ATTTACGACACAGCTGTAATATATAGTGTTTAGTTAGAGTTGGGCAACATGATATTTAT 6600
OY 578 -----IleGlyThrGlnTyrPheLysProGluAspLeuValAspIleIle 591
DB 6601 TTTCGAGAAACATATACATTTGAGACTGATGCG-----ATATATGATATAGGAA 6648
OY 592 ArgMetGluAspLysLysGluValIleProValThrHisAsnLeuThrLeuArgGlyThr 611
DB 6649 AATGAAAGTATTAATATTTATTTCAATCCAGAAACT-----AAAAAGCA 6693

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OY 612 ValThrGlyLeuAlaGlyAspArgThrLysAspPheHisPheGlu----- 626
DB 6694 TCGAAAGGATTAATTAATTTATGATCATATAAATATTTATTTGATGACAGAGGCAATAG 6753
OY 627 -----IleGluLeuLysAsnAsnLysGlnGluLeuLeuSerGlnThrValLys 642
DB 6754 AGACGGGCTATATCATATTGTAATAATTAATTAATTTACTT----- 6795
OY 643 ThrAspLysThrAsnLeuGluLupheLysAspGlyLysAlaThrIleAsnLeuLys----- 660
DB 6796 -----AATGAAATGCTGAATAATGCAATTTGCTTATATAATTAATGAAAGATGTTTC 6849
OY 661 ---HisGlyLysSerLeuThrLeuGln-----GlyLeuProGluGlyTyrSer 675
DB 6850 TATTTTGGGAAAGATGCTGTCTACGATGCGATTTGATTAATTAATACACAGATGATTTAA 6909
OY 676 TyrLeuValLysGlu 680
DB 6910 TACTTTCACATCA 6924

RESULT 15
US-09-070-927A-167
; Sequence 167, Application US/09070927A
; Patent No. US20020120116A1
; GENERAL INFORMATION:
; APPLICANT: Charles A. Kunsch
; Steven Barash
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 982
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 Inch, 1.4MB storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,927A
; FILING DATE: 04-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/046,655
; FILING DATE: 1997-05-16
; APPLICATION NUMBER: 60/044,031
; FILING DATE: 1997-05-06
; APPLICATION NUMBER: 60/066,009
; FILING DATE: 1997-11-14
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenley K. Hoover
; REGISTRATION NUMBER: 40,302
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 167:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19031 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 167:
US-09-070-927A-167

Alignment Scores: 0.0322 Length: 19031
Pred. No.: 139.00 Matches: 158
Score: 34.14% Conservative: 109
Percent Similarity: 34.14%

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Db 3232 GATMAAAGGATCCATCAATACACACCATATCATCATCAATCCCTAAA 3291  
Qy 690 -----ValasSerGlnIuValaIasnaIaThValSerLysThr 703  
Db 3392 AAACCTTTGACATGTCGTAATGCAAAAGCCGATTCGTCGGTGATGCAACGCTAT 3351  
Qy 704 GylIeThrSerAspGluThrLeuAlaPheGluAsnAsn 716  
Db 3352 CAATCACTAAAGATMAAGACAGCTTGATTCGAAACAAAC 3390  
RESULT 14  
US-10-011-366-9  
: Sequence 9, Application US/10011366  
: Publication No. US20030054493A1  
: GENERAL INFORMATION:  
: APPLICANT: Williams, James A.  
: Kink, John A.  
: TITLE OF INVENTION: IDENTIFICATION OF NEUTRALIZING EPITOPES  
: OF TOXIN A AND TOXIN B FOR THE TREATMENT OF C. DIFFICILE  
: DISEASE  
: NUMBER OF SEQUENCES: 22  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Medien & Carroll  
: STREET: 220 Montgomery street, suite 2200  
: CITY: San Francisco  
: STATE: California  
: COUNTRY: United States of America  
: ZIP: 94104  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatentIn Release #1.0, Version #1.30  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/10/011,366  
: FILING DATE: 16-No. US20030054493A1-2001  
: CLASSIFICATION: <Unknown>  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US/08/957,310  
: FILING DATE: 23-OCT-1997  
: APPLICATION NUMBER: US 08/329,154  
: FILING DATE: 24-OCT-1994  
: APPLICATION NUMBER: US 08/161,907  
: FILING DATE: 02-DEC-1993  
: APPLICATION NUMBER: US 07/985,321  
: FILING DATE: 04-DEC-1992  
: APPLICATION NUMBER: US 07/429,791  
: FILING DATE: 31-OCT-1989  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Ingolia, Diane E.  
: REGISTRATION NUMBER: 40,027  
: REFERENCE/DOCKET NUMBER: OPHD-01121  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (415) 705-8410  
: TELEFAX: (415) 397-8338  
: INFORMATION FOR SEQ ID NO: 9:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 7101 base pairs  
: TYPE: nucleic acid  
: STRANDEDNESS: single  
: TOPOLOGY: linear  
: MOLECULE TYPE: DNA (genomic)  
: FEATURE:  
: NAME/KEY: CDS  
: LOCATION: 1..7098  
: SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
US-10-011-366-9

Alignment Scores:  
Pred. No.: 0.00756 Length: 7101  
Score: 139.00 Matches: 154  
Percent Similarity: 30.57% Conservative: 86

Best Local Similarity: 19.62% Mismatches: 249  
Query Match: 3.52% Indels: 296  
DB: 14 Gaps: 38  
US-09-494-297-2 (1-757) x US-10-011-366-9 (1-7101)  
Qy 83 ProTyTyTyLysGlnPheArgValAlaHis----- 92  
Db 4897 CCATATTTCATTAGTTTAAATACACTGAAACCTAATTATATCTTATATGTAGCAATAGA 4956  
Qy 93 -----AspLeuArgValAsnLeuGluGlySerAspSerTyGlnValTyr 107  
Db 4957 CAATAATATGATAGTGTGAACCAAAATTATGATTTAGATGATGAGATATATCTTCACT 5016  
Qy 108 CysPheAsnLeuLysValaPheProLeuGlySerAspSerValLysTyrTyr 127  
Db 5017 GTTATCAATTTCTCTCAAAAGTACTTTATGGAATAGACACTGTGTGTAATAA----- 5070  
Qy 128 LysLysHisAspGlyLysThrLysPheGluAspTyrAlaMetSerProArgLThr 147  
Db 5071 -----GTTGTAATTTCCACCAATATTTAT 5094  
Qy 148 GlyAspGluLeuAsnGlnLysLeuArgAlaValMetTyrAsnGlyHisProGln----- 165  
Db 5095 ACAGATGAAATAATATATACCGCTGTATATGAAACAATAATACTTATCCGAAATTAT 5154  
Qy 166 -----AsnAlaAsnGlyIleMetGluGlyLeuGluProLeuAsnAlaIleArgValThr 183  
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Qy 184 GlnGluAlaValTyrTyrTyrSerAspAsnAlaProIleSerAsnProAspGluSerPhe 203  
Db 5212 ATACGATATGATG-----ACTATGATGTAATGATTTT 5247  
Qy 204 LysArgGluSerGluSerAsnLeuValSerThrSerGluLeuSerLeuMetArgAla 223  
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Qy 224 LeuLysGlnLeuIle-----AspProAsnLeuAlaThrLysMetProLysGln 239  
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Qy 240 ValProAspAspPheGlnLeuSerIlePheGluSerGluAspLysGlyAsp----- 256  
Db 5344 -----TTTACTTACGTAGTAACAAGAGTACCTGTA 5376  
Qy 257 -----LysTyrAsnLysGlyTyrGlnAsnLeuLeuSer 267  
Db 5377 AGTGAAATATCTTATCATTTACACTTCATAT-----TATGAGATGATGATTTAT 5427  
Qy 268 Gly-----GlyLeuValProThrLysProProThrProGlyAspProPromePro 284  
Db 5428 GGCATGATTTGGGCTGAGTT----- 5448  
Qy 285 ProAsnGlnProGlnThrThrSerValLeuIleArgLysTyrAlaIleGlyAspTyrSer 304  
Db 5449 -----TCTTTATATATAGCAAAATTTTATTAATACTTGA 5487  
Qy 305 LysLeuLeuGluGlyAlaThrLeuGlnLeuThrGlyAspAsnValAsnSerPheGlnAla 324  
Db 5488 ATGATGGTATCTGGA-----TTAATATATATTAATGATTCATTTATTTAAACCA 5541  
Qy 325 ArgValPheSerSerAsnAspIleGlyGluArgIleGluLeuSerAspGlyThrTyrThr 344  
Db 5542 CCAGTA-----AAATATTTGATTAACGCGATTTGTGACTGAGCGATATAATACTAC 5595  
Qy 345 LeuThrGluLeuAsnSerProAlaGlyTyrSerIleAlaGluProIle----- 360  
Db 5596 TTTATATCAATTAATGTTGAGCTGCT-----TCAATTGAGAGAGCAATATATGATGACAAA 5652  
Qy 361 -----ThrPheLysValGluAlaGly 367  
Db 5653 AATTATTATTTCACCAAAAGTGAGTGTACAAACAGGTGATTTTATAGAGAGATGGA 5712

LOCATION: (1)...(3504)  
US-09-815-242-7425

**Alignment Scores:**

Pred. No.:	0.00239	Length:	3504
Score:	139.50	Matches:	136

Percent Similarity:	34.50%	Conservative:	110
Best Local Similarity:	19.07%	Mismatches:	282
Query Match:	3.54%	Indels:	185
DB:	9	Gaps:	32

US-09-494-297-2 (1-757) x US-09-815-242-7425 (1-3504)

[illegible]

QY	359	ProIlethrpheIysValGluAlaGlyLysValIYThrIleIleAspGlyLysGlnIle	378
Db	2344	GCTATT---TTTGATCTCAATTCTTAATGGGTGAAMAACGTGGAT---	2388
QY	379	GIuAsnProAsnLysGluIleValGluProGlySerValGluAlaTYrAsnAspPheGlu	398
Db	2389	---CCTTGG-----GGTAAACTTTTCCGA	2412
QY	399	GIuPheSerValLeuThrThrGlnAsnTYrAlaLysPheTYrTYrAlaLysAsnLysAsn	418
Db	2413	AAAACGTTTAAAGCAATCGGTCCAAAC---	2439
QY	419	GlySerSerGlnValValTYrCysPheAsnLAspLeuLys-----	432
Db	2440	-----TGCATTGACACTTATACCGTGTATTGAAAGCCGTTCAATGACCGTTTC	2487
QY	433	-----SerProAspSerGIuAspGlyLysThrMetThrProAspPhe	448
Db	2488	AGGGAAGCGCTTCAACCAACGCAAGCTTAATGAAGTATCAAAAGTCCAGCGAT---	2544
QY	449	ThrThrGlyGluValLysTYrThrHisIleAlaGluAspLeuPheLysTYrVal	468
Db	2545	-----CGCTACAGACGCTTAACGATACAGAATCCACCATGTATAAACG	2589
QY	469	LysProAlaGspThrAspProAspThrPheLeuLysHisIleLysValIleGluLys	488
Db	2590	AAAATCGGTTGGACGTATGT-----TTGAAAAAC-----AAACGATT-----	2628
QY	489	GlyTYrAlaGlyLysGlyGlnAlaIleGluTYrSerGlyLeuThrGluThrGlnLeu---	507
Db	2629	-----AAAATGAAGAAATCGCCAGAAAGCCGATCGAGCGCGTAAAGTTGGCC	2676
QY	508	-----ArgAlaAlaThrGlnLeuAlaIleTYrTYr-----PheThrAspSer	521
Db	2677	TTGTATGCCGCTTTAAACAACATGCGTTATTGGATTAATAATTATGAACAGCA	2736
QY	522	AlaGluLeuAspLys-----AspLys-----LeuLysAspTYrHisGly	534
Db	2737	TCTCATATTGCCCAAAATTTTCCCGGATAAAGCGCGCAATGTGGTGATCAATACGTGT	2796
QY	535	PheGlyAspMetAsnAspSerThrLeuAlaValAlaLysIleLeuValGluTYrAlaGln	554
Db	2797	GTGGTAAATGGTAAGAGATTTTAAAGCGCTGTGTAAACCGATTTTATTTTCGATTTTAAAGTTGG	2856
QY	555	AspSerAsnProProGlnLeuThrAspLeuAspPhePheIleProAsnAsnLysTYr	574
Db	2857	ATCTCA---CCCAATCAGCGCTTACCCTTATATTATGTATGTATCGGGAACCGCGTAT	2913
QY	575	GlnSerLeuIleGlyThrGlnTYrHisProGlnAspLeuValAspIleIleArgMetGlu	594
Db	2914	AACGCTATCAGCGGCTAT-----GGCGTCAACCTTTCAGAGAGCAT	2955
QY	595	AspLysLysGluValIlePro-----ValIYThr	603
Db	2956	TATAAAGATTAATGCATTACTAGGAAGACAGATTTTTCATATTATTAGCATTTTCCAC	3015
QY	604	HisAsnLeuThrLeuAlaGlyLysThValThrGlyLeuAlaGlyAspArgThrLysAspPhe	623
Db	3016	CATAAAGCTATTGGAAAAAATTACAAAACCTCTCTCGGCAAAAGAGCCGCCGA-----	3069
QY	624	HisPheGluIleGluLeuLysAsnLysGlnGlnLeuLeuSerGlnThrValLysThr	643
Db	3070	-----ATGCGCTTTCAGCGAAGACCTTTAAAGACACTCTGTATGCTTTGGCAAAAGATTG	3120
QY	644	AspLysThrAsnLeuGluPheLysAspGlyLysAlaThrIleAsnLeuLysHisGly---	662
Db	3121	GCCGATATTGCACCTGAACATATAGAGTGGGAAATGCAACAAACGTTTAAACATAACTTA	3180
QY	663	---GluSerLeuThrLeuGlnGlyLeuProGluGlyTYrSerTYrLeuValLysGluThr	681
Db	3181	CTAGAGATGCCGAATATGGAGGCTAT-----TATGATGTGATCCAAATGAADAAG	3231
QY	682	AspSerGlnGlyTYrLysValLys-----	689

Db 874 ACAAGCCAAAAGGTGCATTACATTAGAACACGATTATGACTCTAATAGAGTTTCAT 933  
 QY 331 -----AspIleGlyValArgIleGlu----- 337  
 Db 934 TTTTCTGGAAAAGTAATTTAGTACAAATATAGAGCCATGCAATGTGGAGATGCT 993  
 QY 338 -----LeuSerAspGlyThrTyrThrIleuThrGluLeuAsnSerProAla--- 352  
 Db 994 ATCGGTTTGGCTTTTACACAGGTGTATTAGTGAACAGGGTTAAACGGTCCGCACATA 1053  
 QY 353 -----GlyTyrSerIleAlaGluProIleThrPheLysValGluAla----- 366  
 Db 1054 GGTATGTGGCTTAACTAGTAAACGA-----TTGGCTTCAATATAGATCTATACACAT 1107  
 QY 366 ----- 366  
 Db 1108 ACATCTACGCCAAATTCATCAGCAAGCCGAACCTGATCTAATGTAGCTGGTGA 1167  
 QY 367 -----GlyLysValTyrThrIleLeuAsp 374  
 Db 1168 GGTCGTTTGGTGCCTTTGTACACAGATAGTATAGTGTGATCAACATATATACATCA 1227  
 QY 375 GlyLysGlnIleGluAsnProAsnLysGluIleValGluProTyrSerValGluAlaTyr 394  
 Db 1228 AGTTCAACAGCTGATATGTCTGCAAAAGTTAATGTTCACCTACAAAC----- 1275  
 QY 395 AsnAspPheGluGluPheSerVal-----LeuThrThrGlnAsn 407  
 Db 1276 AACACGTTCCAAAGTTTGTATATATATATATATATATATATATATATATATATAT 1335  
 QY 408 TyrAlaLysPheTyrTyrAlaLysAsn-----LysAsnGlySerSer 421  
 Db 1336 TATGACAGTCAAAACATGACACGTAATATTTCAGATTGGATTGGAAAGGTGATACGACC 1395  
 QY 422 GlnValValTyrCysPheAsnAlaAspLeuLysSerProProAspSerGluAspGly 441  
 Db 1396 AACTTTTCATTATCATGATGACAGCC-----TCAACAGGTGGC 1431  
 QY 442 LysThrMetThrProAspPheThrThrGlyValLysTyrThrHisIleAla----- 459  
 Db 1432 GCGCAATTTTACACAAGTACAAATTTGGAACTTGCATATACAGAACTGCTGTACCA 1491  
 QY 460 -----GlyTyrAspLeuPheLysTyrThrValLysPro 470  
 Db 1492 CAATGATACATGTTGATGTACACAGGTAACATATATAT----- 1533  
 QY 471 ArgAspThrAspProAspThrPheLeuLysHisIleLysLysValIle----- 486  
 Db 1534 -----CCCCCAAAAACATATTCTGAAATGTGTGCAAGTCGTCGACAAATCGATAT 1584  
 QY 487 -----GluLysGlyTyrArg-----GluLysGlyGlnAla 496  
 Db 1585 CACAAATCTGCATGACTGCTAAAGATATTAACACACATCTGCAATGTTCAATATGCA 1644  
 QY 497 IleGluTyrSerGlyLeuThrGluThr-----GlnLeuArgAlaIleThrGlnLeuAlaIle 515  
 Db 1645 TCACCTATATATGATACAAATTAACGTAAATATGACGATGCTGGACATTCAGTGCA 1704  
 QY 516 TyrTyrPheThrAspSerAlaGluLeuAspLysAspLysLeuLysAspTyrHisGlyPhe 535  
 Db 1705 TATATATTTTACT----- 1716  
 QY 536 GlyAspMetAsnAspSerThrLeuAlaValAlaLysIleLeuValGluTyrAlaGlnAsp 555  
 Db 1717 ---GATGTAAAGCACCAACGTAACGTAGCAATCAAAACATTTGAAGTGGTAAACA 1773  
 QY 556 SerAsnProGluLeuThrAspLeuAsp----- 565  
 Db 1774 ATGATATCTATTGTGTGACTACACAGATATATGTTACAGGAGCTGTGACAAATACAGTT 1833  
 QY 566 PhePheIleProAsnAsnLysTyr-----GlnSerLeuIleGlyThrGln 581  
 Db 1834 ACAGATTACCAAGCGGATTATAGTATAGTACCAAGAAATTCATCATTTGGGACACCA 1893

QY 582 TrpHis---ProGluAspLeuValAspIleIleLeuArgMetGlu-----AspLysLysGlu 598  
 Db 1884 ACAAAATTTGGTCAATCACTACAGCTGACAGTACTATCTACTGACCAAGCAAAATTAACAAATCG 1953  
 QY 599 ValIleProValThrHisAsnLeu-----ThrLeuArgLysThrValThrGlyLeuAla 616  
 Db 1954 ACGACAACTTTTACAAATATATGTTGGATATACAGACACCAACAGTGACCCACATA--- 2010  
 QY 617 GlyAspArgThrLysAspPheHis-----PheGluIleGluLeuLysAsn 631  
 Db 2011 GGAGATAAATCATCAGAAAGTTTTCCTCCAAATATCCAGCATTAATATATGCTACACAGAC 2070  
 QY 632 AsnLysGlnIleLeuSerGlnThrValLysThrAspLysThrAsnLeuGluPheLys 651  
 Db 2071 AATAGTGTATGCAATACAAATACACTCACAGATTCGCCGTGCTGATTACATTC--- 2127  
 QY 652 AspGlyLysAlaThrIleAsnLeuLysHisGlyLeuSerLeuThrLeuGlnGlyLeuPro 671  
 Db 2128 ---GATACCACAAAATAT-----ACTATATAGTGTACACCA 2160  
 QY 672 GluGlyTyr-----SerTyrLeuValLysGluThrAspSerGluGlyTyrLysVal 688  
 Db 2161 ACAAAACATTTGCTACAGTACTATTACATCGTTCTCTACAGATGCGAGGTGAACAAACG 2220  
 QY 689 LysValAsn---SerGlnGluValAlaAsnAlaThrLysSerLysThrGlyIleThrSer 707  
 Db 2221 ACAACACTTTTAATATATAGAAGTACAAAGAAATACATGATGATTCGTTACCAATCG 2280  
 QY 708 AspGluThr 710  
 Db 2281 GGAAGTACC 2289

RESULT 13  
 US-09-815-242-7425  
 : Sequence 7425, Application US/09815242  
 : Patent No. US20020061569A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Haselbeck, Robert  
 : APPLICANT: Ohlson, Karl L.  
 : APPLICANT: Zyskind, Judith W.  
 : APPLICANT: Wall, Daniel  
 : APPLICANT: Trawick, John D.  
 : APPLICANT: Carr, Grant J.  
 : APPLICANT: Yamamoto, Robert T.  
 : TITLE OF INVENTION: Identification of Essential Genes in  
 : FILE REFERENCE: ELITRA.011A  
 : CURRENT APPLICATION NUMBER: US/09/815,242  
 : PRIOR FILING DATE: 2001-03-21  
 : PRIOR APPLICATION NUMBER: 60/191,078  
 : PRIOR FILING DATE: 2000-03-21  
 : PRIOR APPLICATION NUMBER: 60/206,848  
 : PRIOR FILING DATE: 2000-05-23  
 : PRIOR APPLICATION NUMBER: 60/207,727  
 : PRIOR FILING DATE: 2000-05-26  
 : PRIOR APPLICATION NUMBER: 60/242,578  
 : PRIOR FILING DATE: 2000-10-23  
 : PRIOR APPLICATION NUMBER: 60/253,625  
 : PRIOR FILING DATE: 2000-11-27  
 : PRIOR APPLICATION NUMBER: 60/257,931  
 : PRIOR FILING DATE: 2000-12-22  
 : PRIOR APPLICATION NUMBER: 60/269,308  
 : PRIOR FILING DATE: 2001-02-16  
 : NUMBER OF SEQ ID NOS: 14110  
 : SOFTWARE: fastseq for Windows Version 4.0  
 : SEQ ID NO 7425  
 : LENGTH: 3504  
 : TYPE: DNA  
 : ORGANISM: Helicobacter pylori  
 : FEATURE:  
 : NAME/KEY: CDS.

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Db      612 -----ACGAAGCC-----TTACGAGC----- 629
Qy      619 AtgthrlYsAspPheHisPheGluIleGluLeuLysAsnAsnLysGlnGluLeuSer 638
Db      630 -----GCAGAAATTACATTGAAGATGTGAAGCAATGTGTGA 671
Qy      639 GlnThrValLysThrAspLysThrAsnLeuGluPheLysAspGlyLysAlaThrIleAsn 658
Db      672 GAAGCAATTACACAGATTAAGTCTGCA----- 698
Qy      659 LeuLysHisGlyLysSerLeuThrLeuGlnGlyLeuProGluGlyTyrSerTyrLeuVal 678
Db      699 -----ACGTAAAGTAGAGCGAGCTGTGCGCGGT---GAATATACGTTA 740
Qy      679 LysGluThrAspSer---GluGlyTyrLys-----ValLysValAsnSerGlnGlu 694
Db      741 GAAGAAACAAAGCCGACGAGAGTTATAGCATTAAGATCAATCAAGTAAACGTA 800
Qy      695 ValAlaAsnAlaThrValSerLysThrGlyIleThrIserAspGluThrLeuAlaPheGlu 714
Db      801 GTAGCAACGAACTGTA----- 818
Qy      715 AsnAsnLysGluProValValProThrGlyValAspGlnLysIleAsnGlyTyrLeuAla 734
Db      819 -----AAACAGACGTGTGTAATGAAGAAAGAAAGAAATTAACAGCGCAATTAGAA 872
Qy      735 LeuIleValIle-----AlaGlyIleSerLeuGlyIle 745
Db      873 ATTCAAAAGTAGATGCTAATGATATATATAAAATTATGACGCGCATGTGTGAATT 932
Qy      746 TTP 746
Db      933 TGC 935

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RESULT 12
US-09-815-242-8615
; Sequence 8615, Application US/09815242
; Patent No. US20020061569A1
GENERAL INFORMATION:
; APPLICANT: Haseibeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trivick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8615
; LENGTH: 7035
; TYPE: DNA
; ORGANISM: Staphylococcus aureus

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(7035)
US-09-815-242-8615
Alignment Scores:
Pred. No.: 0.00214 Length: 7035
Score: 144.50 Matches: 153
Percent Similarity: 31.638 Conservative: 101
Best Local Similarity: 19.058 Mismatches: 238
Query Match: 3.66% Indels: 251
DB: 9 Gaps: 38
US-09-494-297-2 (1-757) x US-09-815-242-8615 (1-7035)
Qy      79 ValAlaGlyHisProTyrTyrLysGlnPheAlaHisAspLeuArgValAsnLeu 98
Db      121 ATAAAGGACATCCATTTATAGTCATAGTATGAGTCAAGAT----- 165
Qy      99 GluGlySerArgSerTyrGlnValTyrCysPheAsnLeuLysAlaPheProLeuGly 118
Db      166 AATCAAGCATTAAGTAAATAAATGACTGGATCGGATGAAGAACGACGCGACTGATCGGC 225
Qy      119 SerAspSerSerValLysLysTyrTyrLysLysHisAspGlyIleSerThrLysPheGlu 138
Db      226 GGGCGTTTCACGGTAAAC-----ATGTTGCATGACCAAC-----CAA 261
Qy      139 AspTyrAlaMetSerProArgIleThrGlyAspGluLeuAsnGlnLysLeuArgAlaVal 158
Db      262 GCTTTGGCGGCTTCGATGACCACTTAACATCTGAATTAATACAAAGTGAACAGTA 321
Qy      159 MetTyrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGluGlyLeuGluProLeuAsn 178
Db      322 -----GTTAAT---CAAAATTCACGACAAATGATGCTCAACATCAACACCGCAT 369
Qy      179 AlaIleArgValThrGlnGluAlaValTyrTyrSerAspAsnAlaProIleSerAsn 198
Db      370 TCCACAGCGTAAACGAAAT-----AGTAGTTCGGTACAAACATCAAT 414
Qy      199 ProAspGluSerPheLysArgLysGluSerAsnLeuValSerThrSerGlnLeuSer 218
Db      415 AGTGACACAGTCTCAAGTGAAGAAAGTCTGAA---AATGTCACTCGCAACATTAAGTACA 471
Qy      219 LeuMetArgGlnAlaLeuLysGlnLeuIleAspProAsnLeuAlaThrLysMetProLys 238
Db      472 ACCAATCAACAA-----GAAAATTGACATCTACATGAAATCAACATCTCAAGAAAT 525
Qy      239 GlnValProAspAspPheGlnLeuSerIlePheGluSerGluAspLysGlyAspLysTyr 258
Db      526 ACTACATCAAGTTGATGATCTAATCTGTAACTCAACTCAAGTACAGAACACCAAT 585
Qy      255 AsnLysGly---TyrGlnAsnLeuLeuSerGlyGlyLeuValProThrLysProProThr 277
Db      586 AATACATCAACAAATCAAGTACTGCATCAATTAACACTTCACAAAGCAACAGCCCACT 645
Qy      278 ProGlyAspProPheMetProProAsnGlnProGlnThrThrSerValLeuIleArgLys 297
Db      646 TCAGCCAC-----TTAAACAAACTACACACACACTCAACTACAGCTCGCGCA 693
Qy      298 TyrAlaIleGlyAspTyrSerLysLeu----- 306
Db      694 GTAAACCTTCGAACCTTCAGTCGTAGTATGTCACATTTGCGTCACGACGACGACA 753
Qy      307 -----LeuGluGlyAlaThrLeuGlnLeuThrGlyAspAsnValAsnSerPheGln--- 323
Db      754 ACCGATTAACGTCTAATACAAATTAACAGTTAATAAAGTAACCTTAACAAATATATGACA 813
Qy      323 ----- 323
Db      814 ACTTCAGTAATGCCACTTATGACCAAGTACAGGGGTCTAAGCTTAACGACAGATACA 873
Qy      324 -----AlaArgValPheSerSerAsn----- 330

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Db 2638 ACATCAACAACAGGTGTCATTAAAGATAAAGATACGATACCTATGACCTGCTTCTAC 2697
QY 529 -----LeuLysAspTyr-----HisGlyPheGly 536
Db 2698 AAMCCGACTTACAACTTAGGTATGTATGGAGATACAAATAAAGCGGTTCOA 2757
QY 537 AspMetAsnAspSerThrLeuAlaValAla-----Lys 547
Db 2758 GATTAAGATGAAGAAGCGCATTTTCAGTGCTAACACTTACGTTAAAGATGAAGAACGACAAA 2817
QY 548 IleLeuValGluTyrAlaGlnAspSerAsnProPro--GlnLeuThrAspLeuAspPhe 566
Db 2818 GTTTTAAACAGAGTTACACAGAGTAAGTAATGTAATATCAATTCACGTGATTTTA----- 2871
QY 567 PheIleProAsnAsnAsnLysTyrGlnSerLeuIleGlyThrGlnThrPheProGluAsp 586
Db 2872 -----AACATGGACACTTATATA----- 2889
QY 587 LeuValAspIleIleArgMetGluAspLysGluValIlePro-----ValThrHis 604
Db 2890 -----GTTGAATTCGAGACACACATCAGCTTATACACCACTTCAGTACTTCT 2937
QY 605 AsnLeuThrLeuArgLys-----ThrValThrGlyLeu-----Ala 616
Db 2938 GGAATATGATCTGAAAAAGATTCCTAATGCTTTAACACACACGCTGTCATTAAGATGCA 2997
QY 617 GlyAspArgThrLysAspPheHisPheGluIleGluLeuLysAsnAsnLysGlnGluLeu 636
Db 2998 GATTAACATGACATTAGCAGTGGTTTC-----TATTAACACCAAAATATAGTTTA 3048
QY 637 -----LeuSerGlnThrValLysThrAspLysThrAsnLeuGlu 649
Db 3049 GGTGATTATGTTGGTACGACAGATAATTAAGACGCAACAGATCAACTCAAGTAAAGAGT 3108
QY 650 PheLysAspGlyLysAlaThrIleAsnLeuLysHisLysGlySerLeuThrLeuGlnGly 669
Db 3109 ATCAAAAGATCTTAAGTACTTTATTAATGAAGAAAAACGCAAGTAATGCAACCACTAAA 3168
QY 670 LeuProGluGlyTyrSerTyrLeuValLysGluThrAspSerGluGlyTyrLysValLys 689
Db 3169 ACAGATCAAAATGCTAATATGCTTGCATTAATTAATGCGTAAATACAAAGTTATT 3228
QY 690 ValAsnSerGlnGluValAlaAsnAlaThrValSerLysThrGlyIleThrSerAspGlu 709
Db 3229 TTT-----GAAAAGCTGCTGGCTTAACACAAACAGCTTACAAATACAGTGAAGATGAT 3282
QY 710 ThrLeuAlaPheGluAsnAsnLysGluProValValProThrGlyValAspGlnLysIle 729
Db 3283 AAGATGCAAGATGGTGGCGAAGTTGACGTAAACAATTACGATCATGATTCACACTT 3342
QY 730 ---AsnGlyTyr 732
Db 3343 GATTAACGATAC 3354

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US-09-494-297-2 (1-757) x US-09-842-552-98 (1-2522)
Alignment Scores:
Pred. No.: 0.000302 Length: 2522
Score: 146.50 Matches: 100
Percent Similarity: 35.14% Conservative: 62
Best local Similarity: 21.69% Mismatches: 112
Query Match: 3.71% Indels: 187
DB: 9 Gaps: 23

US-09-842-552-98
QY 305 LysLeuLeuGluGluAlaThrIleGluLeuThrGlnLysAsnValAsnSerPheGlnAla 324
Db 57 CAATCTTACCAGGTGCAAAATTTGATGCTTATCATGATTAAGATGCGAAAGTTGCGAACA 116
QY 325 ArgValPheSerSerAsnAspIleGlyGluArgIle-----GluLeuSerAspGlyThr 342
Db 117 ATTGTT-----ACAGATGATTAAGGTGCAAGCTTATCGAACAACCTTCAGTTGCAAGC 170
QY 343 TyrThrLeuThrGluLeuAsnSerProAlaGlyTyrSerIle---AlaGluProIleThr 361
Db 171 TATCACTTAAAGAAAGAGAGCAAGCCGAAAGGATGATCAATATCATCTACTGCTCAGTTCT 230
QY 362 PheLysValGluAlaGlyLysValTyrThrIleLeuAspGlyLysGlnIleGluAsnPro 381
Db 231 GTTCATGTAGAGGCTAATTAAGTAGTGACT-----GTAGATGTGCTG 272
QY 382 AsnLysGluIleValGluProTyrTyrSerValGluAlaTyrAsnAspPheGluPheSer 401
Db 273 AATTAAGATATCCCGGAAAAAGTAAACA-----GGTCAATTTGAA 311
QY 402 ValLeuThrThrGlnAsnTyrAlaLysPheTyrTyrAlaLysAsnLysAsnGlySerSer 421
Db 312 GTGGTGAAGTAGTAGTCAAAATGATATA-----ACGAAATGTTATACAGTGGCGAA 362
QY 422 GlnValValTyrCysPheAsn-----AlaAspLeuLysSerProProAspSerGlu 438
Db 363 TTCACATGATTAAGATGCAAAAGAGTACAGCACTGAAA-----ACAGGT 410
QY 439 AspGlyLysTyrThrMetThrProAspPheThrThrGlyValLysTyrThrHisIle 458
Db 411 GAGAGTGGAAAGATGATGTCACCGAAATTAACCGCTAGGTAAA----- 452
QY 459 AlaGlyArgAspLeuPheLysTyrThrValLysProArgAspThrAspProAspThrPhe 478
Db 453 -----TACACAGTGAAA----- 464
QY 479 LeuLysHisIleLysValIleGluLysGlyTyrArgGluLysGlyGlnAlaIleGlu 498
Db 464 ----- 464
QY 499 TyrSerGlyLeuThrGlnThrGlnLeuArgAlaAlaThrGlnLeuAlaIleTyrTyrPhe 518
Db 465 -----GAAACGAAAGCACACGCGGCTACACAGCTTTCAGATAAAGATGCG 509
QY 519 ThrAspSerAlaGluLeuAspLysAspLysLeuLysAspTyrHisGlyPheGlyAspMet 538
Db 510 AAGATCACAATTCACAAACGAGAAAGAA----- 536
QY 539 AsnAspSerThrLeuAlaValAlaLysIleLeuValGluTyrAlaGlnAspSerAsnPro 558
Db 537 -----GTAGTAAAGTAGAGGCACAA----- 557
QY 559 ProGlnLeuThrAspLeuAspPhePheIleProAsnAsnAsnLysTyrGlnSerLeuIle 578
Db 558 -----AACCAAAA-----ATCTTA 572
QY 579 GlyThrGlnThrPheProGluAspLeuValAspIleIleArgMetGluAspLysGlu 598
Db 573 GGTTCt-----CTACAAATATTATTAATAATGGATGATGAATGAATCAA 611
QY 599 ValIleProValThrHisAsnLeuThrLeuArgLysThrValThrGlyLeuAlaGlyAsp 618

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OY 26 PheThrValThrLeuValGlyValPheLeuMetIlePheAlaLeuValThrSerMetVal 45
Db 682 TGAATACAAAGA-----ATGCGTATGACAGACTGATCAGCATCATCAACA 726
OY 46 GlyAlaIleYsthrValPheGlyLeuValGlySerSerThrPro-----59
Db 727 GAGGCTAAAGTTATGATTAATGATTAATCAATCAAAATCAACATTAACGTGCTTGATGCA 786
OY 60 -----AsnAlaIleAsnPro-----AspSerSerSerGlyIleArgTrpGly 74
Db 787 GATAAACAAATTAATTCCTACACGCCCAAGATTATTATCATTTAAATCACAATTAACA 846
OY 75 TyrGlySerTyrValArgGlyHisProTyrTyrGlyGlnPheArgValAlaHisAspLeu 94
Db 847 GTGATGACAAAGTTAATCAGGTGATTTATTC-----879
OY 95 ArgValAsnLeuGlySerArgSerTyrGlnValTyrCysPheAsnLeuLysGlyAla 114
Db 880 -----ACAATTAAATACACAGATACAGTACAGTATGATGATGATCCGGAAGATATT 933
OY 115 PheProLeuGlySer-----AspSerSerValLysIstTrpTyrLysHis 130
Db 934 AAAAATATTGGTATTTAATTAAGATCCAAATTAATGGTGAACAATTCGACCTGCAAAACAT 993
OY 131 AspGly-----IleSerThrLysPheGlyAspTyrAlaMetSerProArgIle 146
Db 994 GATACGTGCAAAATATTATTAATTCATATACATTATACAGTTATGTT-----1038
OY 147 ThrGlyAspGlyLeuAsnGlyLysLeuArgAlaValMetTyrAsnGlyHis-----163
Db 1039 -----GATCGATTTAATCTCTGACAAATGGGAATTAATTAATTAATTAATGATGCT 1092
OY 164 -----ProGlnAsnAlaAsnGlyIleMetGlyLeuGlnProLeuAsnAlaIle 180
Db 1093 GATACAAATCTCTGTTAGTAAACCATGTTGAGTTAATGTTACGATAGCTATTAACA 1152
OY 181 ArgValThrGlnGluAlaValTrpTyrTyrSerAspAsnAlaProIleSerAsnProAsp 200
Db 1153 ACAAAAACAACATGCTAATCATCAATATCCAGATTATGTTAATGAGAAATATCAAT 1212
OY 201 GluSerPheLysArgGlySerGlySerAsnLeu-----211
Db 1213 GGATCAGCGCTCACTGAACACATTTCCACATGTTGGAATTAAGAAATCCAGGCTACTAT 1272
OY 212 -----ValSerThrSerGlnLeuSerLeuMetLargGlnAlaLeuLys---225
Db 1273 AAACAACAGATTATGTTAATTCATCGGAATTTCTTTAACAATGCCAAACCTAAAGTT 1332
OY 226 -----GlnLeuIleAspProAsnLeuAlaThrLysMetProLysGlnValProAsp 242
Db 1333 CAAGCTTACCACCTCAAGTATCTATATATTCGGGCAAAATTAATTAAGATGTAACAGAT 1392
OY 243 AspPheGlnLeuSerIlePheGlySerGlyAspLysGlyAspLysTyrAsnGlyTyr 262
Db 1393 -----ATTAATAATATATCAAA---GTTCTTAAGGTTATATACATTAATTAAGGATAC 1440
OY 263 GlnAsnLeuSerGlyGlyLeuValProThrLysProProThrProGlyAspProPro 282
Db 1441 GAT-----GTGATACTAAAGACTTACA-----1464
OY 283 MetProProAsnGlnProGlnThrThrSerValLeuIleArgLysTyrAlaIleGlyAsp 302
Db 1465 -----GATGTACAATCAATCACTTGCAGAAATTAACATATGCGCAGC 1506
OY 303 TyrSerLys-----305
Db 1507 AACCAATAGCGCTGTTATGATTTGGAAAATGCAGATTCGCTTATGTTAATGCTTAAT 1566
OY 306 -----LeuLeuGlyGlyValThrLeuGln 313
Db 1567 ACAAAATTCCATATATCAAAATAGCGAAAGCCCAACACTTGTTCAAAATGCTACTTATCT 1626
OY 314 LeuThrGlyAsp-----317

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Db 1627 TCAACAGGTAAATAAATCCGTTTCTACTGCGCAATGCTTTAGATTACTAATAACCAAGT 1686
OY 318 -----AsnVal 319
Db 1687 GCGGAGCTGCGTCAGAAGTATATATAAATTGTAACACTAGCTATGGAGACTACTAATAA 1746
OY 320 AsnSerPheGln-----AlaArgValPheSer 328
Db 1747 AACGGTTCACAAATTAGAGAGAAAAAGCGCTTGCAATGTAACTGTAACGTATTTGAT 1806
OY 329 SerAsn-----AspIleGlyGluArgIleGlyLeuSerAspGlyThrTyrThrLeu 345
Db 1807 AATAATACAAATACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1866
OY 346 ThrGlyLeu-----AsnSerProAlaGlyTyrSer 355
Db 1867 CCAAACTTACCTAATGAGATTACCGTGTAGAATTTTCAAACTTAACCAAAAGTTATGAA 1926
OY 356 IleAlaGlu-----358
Db 1927 GTAAACCCCTTCAAAACAGGTAAATTAACGAAGATTGATTTCAACGGCTTATCTCAGTT 1986
OY 358 -----358
Db 1987 ATTACAGTTAATGCAAAAGATTAATCTATCTGACAGCTAGGTATTTAACAACCTAATAC 2046
OY 358 -----358
Db 2047 AACTATGACTATGCTCTGGGAAGATACAAATTAATGATTCACAGACCAAGATGAA 2106
OY 359 -----ProIleThrPheLysValGluAlaGlyLysValTyr 370
Db 2107 AAGGTATATCTGCGTAAACGGTATACATTAAAGATGAAGAACGGTACGTGTTAAAAACA 2166
OY 371 -----ThrIleLeuAspGlyLys-----Gln 377
Db 2167 GTTACAACAAGACCGTATGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATAA 2226
OY 378 IleGluAsnProAsnLysGlyIleValGluProTyrSerValGluAlaTyrAsnAspPhe 397
Db 2227 GTTGAATTACTACACCAAGAGCTATACACCCACATGATACATGCTGATGCGCAGATT 2286
OY 398 GluGluPheSer-----ValLeuThrThrGlnAsnTyr-----408
Db 2287 GAAAAAGACTCTAATGTTTAAACACACACAGGCTTATTAATGCTGCTGTAACATGACA 2346
OY 409 -----AlaLysPheTyrTyrAlaLysAsnLysAsnGlySerSerGlnValTyrCys 426
Db 2347 TTAGATAGTGGATTCTACAAACACCAAAATATTAATTAATTAATTAATTAATTAATTA 2406
OY 427 PheAsnAlaAspLeuLysSerProProAspSerGluAsp-----GlyGlyLysThr 443
Db 2407 ACAAAATTAAGAGTGTAAAGCAG-----GATTTCAACTGAAAGAGTATTCGACGCTTACA 2460
OY 444 MetThrProAspPheThrThrGlyGluValLysTyrThrHisIleAlaGlyArgAsp---462
Db 2461 GTTACATTGAAAAAATGAAACGCTGAAGTTTACAAACACATTAACATTAAGATGGT 2520
OY 463 LeuPheLysTyrThrValLysProArgAspThrAspProAspThrPheLeuLysHisIle 482
Db 2521 AATATATCAATTTACT-----2535
OY 483 LysLysValIleGlyLysGlyTyrArgGlyLysGlyGlnAlaIleGlyTyr-----499
Db 2536 -----GATTTAGAAAATGCAACTTATTAAGTTGAATTCAGAAACACCA 2577
OY 500 SerGlyLeuThrGluThrGlnLeuArgAlaAlaThrGlnLeuAlaIle---TyrTyrPhe 518
Db 2578 TCAGGTTACACACCAACAGATAGGTTACAGACATGAGAGGTATTAATTCATTAATGCT 2637
OY 519 ThrAspSerAlaGlyLeuAspLysAspLys-----528

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OY	378	IIeGIuAsnProAsnLysGIuIIeValIuProfYSerValGIuAlaTYrAsnSph	397
Db	2227	GTGGATTACTACACCGAAGCGCTATACACCGACTACAGTAACATCTGGTAGCGACATT	2286
OY	398	GIuGIuPheSer-----ValLeuThrThcIuInsntYr	408
OY	409	-----AlaIysPheTYrAlaIysAsnLysAsnLysSerGlnValValTYrCys	426
Db	2287	GAAGAAAGCTCATATGTTTAAACAACAACAGCGTTATTAATGCTGCTGATPAACATGACA	2346
OY	427	PheAsnAlaAspLeuLysSerProProAspSerGIuAsp-----GlyGlyLysThr	443
Db	2407	ACAATTAAGATGGTGAATACAG-----GATTCACACTGAAAAAGATATTTCAGCGCTACA	2466
OY	444	MetThrProAspPheThrThcGlyGIuValLysTYrThrHisIIeAlaGlyArgAsp---	462
Db	2461	GTTACATTGAAAAATGAAGAACGGTCAAGTTTACAAACACACTAAACAGATAAAGATGCT	2520
OY	463	LeuPheTYrTYrValLysProArgSphThrAspProAspThrPheLeuLysHisIle	482
Db	2521	AAATATCAATTACT-----	2535
OY	483	LysLysValIIeGIuLysGlyTYrArgGIuLysGlyGlnAlaIIeGIuTYr-----	499
Db	2536	-----GCATTGGAAAAATGCAACTTAAAGTTGAATTCGAAACACCA	2577
OY	500	SerGlyLeuThrGIuThrGlnLeuArgAlaAlaThrGlnLeuAlaIle---TYrTYrPhe	518
Db	2578	TCAGGTTACACACCAACCAAGTAGTGTTACAGGAAGTGAAGATGATTCAAATGCT	2637
OY	519	ThrAspSerAlaGIuLeuAspLysAspLys-----	528
Db	2638	ACAATCAACAACAGCGTCTATTAAAGATTAAGATAACGATACTATTGACTCGGTTTCTAC	2697
OY	529	-----LeuLysAspTYr-----HisGlyPheGly	536
Db	2698	AAACCGACTTACAACCTTAGCTAGCTATGTATGGAGATACAAATTAATAAACGGTGTCCA	2757
OY	537	AspMetAsnAspSerThrLeuAlaValaIa-----Lys	547
Db	2758	GATTAAGATGAAAGGCGCATTTACAGGTGAACAGTTACGTTAAAGATGAAGAACACAA	2817
OY	548	IIeLeuValGIuTYrAlaGlnAspSerAsnProPro---GlnLeuThrAspLeuAspPhe	566
Db	2818	GTTTTTAAAAACAGTTACACACAGATGAATAATGTAATTCATTCACATTCAGATTTA-	2871
OY	567	PheIIeProAsnAsnAsnLysTYrGlnSerLeuIIeGlyThrGlnTYrPheAsnProGIuAsp	586
Db	2872	-----AACATTCGCAACTTATTAATAA-----	2889
OY	587	LeuValaIleAspIIeIleArgMetGIuAspLysLysGIuValIIePro-----ValThrHis	604
Db	2890	-----GTTGAATTGGAAGACACACATCAGATTATACACCAACTTCAGTAACCTCT	2937
OY	605	AsnLeuThrIleuArgLys-----ThrValaIleThrGlyLeu-----Ala	616
Db	2938	GGAAATGACTGAAGAAAGATTTCAATGCTTTAAACAACACAGCGTCAATTAAGATGCA	2997
OY	617	GlyAspArgTYrThLysAspPheHisPheGlyIIeGlnLeuLysAsnAsnLysGlnGIuLeu	636
Db	2998	GATAACATGACATTAAGACAGTGGTTTC-----TATTAATAACACCAAAATATAGTTTA	3048
OY	637	-----LeuSerGlnThrValLysTYrThrAspLysThrAsnLeuGIu	649
Db	3049	GGTATATTGTTGTCGTACGACAGTAATTAAGACGCAACAAAGATTCACAACTGAAGAAAGCT	3108
OY	650	PheLysAspGlyLysAlaIleThrIIeAsnLeuLysHisGlyGlnSerLeuThrLeuGlnGly	669
Db	3109	ATGCAAGATGTTGAAGTACTCTTTTAAATGATAAAAGCGCAAGTATGTGAACAACATAA	3168

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OY      670  LeuProGluucllyrlyserlyleuVallylsgluThrAspSerglucllyTyrlylVallyls 68
Db      3169 ACACATGATAAAATGTAATAACTGCTTTGATTAATTAGATAGCGTAATATACAAAGTATTT 322
OY      690  ValAsnSerIngluValAlaAsnAlaThrValSerlystHrglyleThSerAspGlu 708
Db      3229 TTT-----GAAAAGCTGCTGGCTTAACACAAACAGTTACAAATACAACTGAAAGATGAT 332
OY      710  ThrLeuAlaPhegluAsnAsnlysgluProvalValProThrglyValAspGlnsile 728
Db      3283 AAAGATACAGATGGTGGCGAAGTGTGACGTAAACAATTACGATCATGATGATTCACACTT 334
OY      730  ---AsncllyTyr 732
Db      3343 GATAACGGATAC 3354

RESULT 10
US-09-815-242-9039
; Sequence 9039, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlssen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wali, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9039
; LENGTH: 4050
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4050)
US-09-815-242-9039

Alignment Scores:
Pred. NO.: 0.000541 Length: 4050
Score: 147.00 Matches: 203
Percent Similarity: 29.28% Conservative: 91
Best Local Similarity: 20.22% Mismatches: 338
Query Match: 3.73% Indels: 372
DB: 9 Gaps: 44

US-09-494-297-2 (1-757) x US-09-815-242-9039 (1-4050)
OY      8  AsnlyleuAsnThrleuAsnThrGlnArGValleuSerlyAsnSer-----LysArg 25
Db      622  AATTCAAAATCTTCAAAAATATGACGATATCATTTTGGCCAAAAGTACGACACTTAAGCT 681

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: PRIOR FILING DATE: 2000-03-21
: PRIOR APPLICATION NUMBER: 60/206, 848
: PRIOR FILING DATE: 2000-05-23
: PRIOR APPLICATION NUMBER: 60/207, 727
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: 60/242, 578
: PRIOR FILING DATE: 2000-10-23
: PRIOR APPLICATION NUMBER: 60/253, 625
: PRIOR FILING DATE: 2000-11-27
: PRIOR APPLICATION NUMBER: 60/257, 931
: PRIOR FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: 60/269, 308
: PRIOR FILING DATE: 2001-02-16
: NUMBER OF SEQ ID NOS: 14110
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 4843
: LENGTH: 4047
: TYPE: DNA
: ORGANISM: Staphylococcus aureus
US-09-494-297-2

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Alignment Scores:
Pred. No.: 0.00054 Length: 4047
Score: 147.00 Matches: 203
Percent Similarity: 29.28% Conservative: 91
Best Local Similarity: 20.22% Mismatches: 338
Query Match: 3.73% Indels: 372
DB: 9 Gaps: 44
US-09-494-297-2 (1-757) x US-09-815-242-4843 (1-4047)

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QY 8 AsnLysLeuAsnThrLeuAsnThrGlnArgValLeuSerLysAsnSer-----LysArg 25
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 622 AATTCAAAATTAAGAAATATATGAGATATATTCCTCCAAAGATACAGACCTTAACGT 681
QY 26 PheThrValThrLeuValAlaValPheLeuMetIlePheAlaLeuValThrSerMetVal 45
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 682 TTGAATACAAAGA-----ATGCGTATGACGACGATACAGCCATCATCATCAAGA 726
QY 46 GlnAlaLysThrValPheGlyLeuValGlnSerSerThrPro-----LysVal 59
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 727 GAGCGTAAATATGTTATATATATATATATATATATATATATATATATATATATATAT 786
QY 60 -----AsnAlaIleAsnPro-----AspSerSerSerGlnIleArgIleArgIle 74
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 787 GATTAATAAATTAATATATATATATATATATATATATATATATATATATATATATAT 846
QY 75 TyrGlnSerThrValArgGlnHisProTyrTyrTyrGlnPheArgValAlaHisAspLeu 94
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 847 GTTGATGACAAAGTTAAATCAGGTGATTTTC----- 879
QY 95 ArgValAsnLeuGlnGlySerArgSerTyrGlnValTyrCysPheAsnLeuLysLysAla 114
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 880 -----ACAATTAATATCTCAGATACAGTATATATATATATATATATATATATAT 933
QY 115 PheProLeuGlySer-----AspSerSerValLysLysIleArgIleArgIle 130
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 934 AAAATATATGATATATATATATATATATATATATATATATATATATATATATATAT 993
QY 131 AspGly-----IleSerThrLysPheGlnAspTyrAlaMetSerProArgIle 146
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 994 GATACGCAAAATATATATATATATATATATATATATATATATATATATATATATAT 1038
QY 147 ThrGlnAspGlnLeuAsnGlnLysLeuAlaValAlaMetCysArgLysHis----- 163
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1039 -----GATCGATTAATATCTCTACAAATGGAATTAATTAATTAATTAATTAATTA 1092
QY 164 -----ProGlnAsnAlaAsnGlnIleMetGlnGlyLeuGlnProLeuAsnAlaIle 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1093 GATACATTCCTGCTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1152
QY 181 ArgValThrGlnGlnAlaValTyrTyrTyrSerAspAsnAlaProIleSerAsnProAsp 200
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Db 1153 ACAAAAAACATCTGAATTCATATATCCAGATATATGTTGTAATGAGAAAAATTCATAT 1212
QY 201 GlnSerPheLysArgGlnSerGlnSerAsnLeu----- 211
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1213 GGATCAGCGCTTACTGATCAAGATGTTTCAATGTTGAAATTAAGAAATTCAGGCTACTAT 1272
QY 212 -----ValSerThrSerGlnLeuSerLeuMetArgGlnAlaLeuLys--- 225
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1273 AAACAAACGATTTATGTAATTCATGCGAAATATCTTTTAAACAATGCCAACTGAAAAAGT 1332
QY 226 -----GlnLeuIleAspProAsnLeuAlaThrLysMetProLysGlnValProAsp 242
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1333 CAAGCTTACCATCTCAAGTATCTTAATATATGCGCAAAATTAATTAAGATTAACAGAT 1392
QY 243 AspPheGlnLeuSerIlePheGlnSerGlnAspLysGlyAspLysTyrAsnLysGlyTyr 252
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1393 -----ATTAATAATATATCAAA---GTTCTTAAGGTTATACATTAATTAAGGATAC 1440
QY 263 GlnAsnLeuLeuSerGlyGlyLeuValProThrLysProProThrProGlyAspProPro 282
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1441 GAT-----GTGAATACTAAAGAGCTTACA----- 1464
QY 283 MetProProAsnGlnProGlnThrThrSerValLeuIleArgLysTyrAlaIleGlyAsp 302
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1465 -----GATGTACAAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1506
QY 303 TyrSerLys----- 305
Db 1507 AACAAATAGCGCTGTTATGATTTTGCATTTGCAATTCAGATTCCTTATGTTAATGCTTAAT 1566
QY 306 -----LeuLeuGlnGlyAlaThrLeuGln 313
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1567 ACAAAATTCCAATATCAAAATATAGCAAGGCCAACAACCTGTTCAAAATGGCTACTTATCT 1626
QY 314 LeuThrGlyAsp----- 317
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1627 TCACACAGTAAATTAATCCGTTTCTACTGGCAATGCTTAAAGATTTACTAATAACCAAGT 1686
QY 318 -----AsnVal 319
Db 1687 GCGGAGCTGCTCAACAGATATTAATTAATTTGTAACGTATGCAAGATCTAATAATAA 1746
QY 320 AsnSerPheGln-----AlaArgValPheSer 328
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1747 AACGGTGTCAAGAAATATAGSAGAAAAAGCGTTGGCAATGTACTGTAATGATTTGAT 1806
QY 329 SerAsn-----AspIleGlyGlnArgIleGlnLeuSerAspGlyThrTyrThrLeu 345
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1807 AATAATACAAATCAAAAGATGAGGAAAGCAGTTACTAAAGAAAGATGGTCTATGATTT 1866
QY 346 ThrGlnLeu-----AsnSerProAlaGlyTyrSer 355
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1867 CCAAACTTACCTAATGAGATTAACGTTAGATTTTCAAACTTCAAAAGGTTATGAA 1926
QY 356 IleAlaGln----- 358
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1927 GTTACCCCTTCAAAACAGCTAATTAACGAAGATTTAGATTCAACCGCTATCTCAGTT 1986
QY 358 ----- 358
Db 1987 ATTACAGTTAATGCAAGATATATCTGACAGCTTAGGTATTTACAAACTTAATATAC 2046
QY 2047 AACTATGTGACTATGTCTGGGAAGATACAAATTAATTAATGTTCCAAAGCAAGATGAA 2106
QY 359 -----ProIleThrPheLysValGlnAlaGlyLysValTyr----- 370
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2107 AAAGGTATATCTGCGCTAACGTTAATCAATTAATTAATTAATTAATTAATTAATTAAT 2166
QY 371 -----ThrIleLeuAspLysLys-----Gln 377
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2167 GTTACAAACAGCGCTGATGCAAAATTAATTAATTTACTGATTTACATTAATGTAATATATA 2226

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Db 1279 ATTGCTAATATTAAAGCTGTGCTAGTGCAGACCTATTATTAAAGAAATAGAGCGCA 1338
QY 253 -----AspLysGlyAspLysTyr-----Asn 259
Db 1339 CGACCGTATACATTTGAGATTAAGAAATATCGTTACTATGAAAGATACAGATTAAT 1398
QY 260 LysGlyTyrGlnAsnLeuSerCylGlyLeu-----ValPro 272
Db 1399 CAGGATATTTTACGACTATTTGAAATGCAAAAGCGATAGAAAAACAAAGATTTTCT 1458
QY 273 ThrLysProProthProGlyAspProMetProProAsnGlnProGlnThrThrSer 292
Db 1459 GCTCAAAAGTTTGGGAGGACCTCAAAAGTGAACA-----ACG 1500
QY 293 ValLeuLeuArgLysTyrAlaIleGlyAspTyrSer----- 304
Db 1501 ATTATATTCAGATTGTCACAAACAGATGACAAATACAAACACACAGTAGACAAACA 1560
QY 305 -----LysLeuLeuGluGlyAlaThrLeuGlnLeuThrGlyAspAsnValAsnSerPhe 322
Db 1561 GAGATTAAAAATTAAGAGATGAGACGACAAAGTGACATGGCTTAATCTT----- 1611
QY 323 GlnAlaArgValPheSerSerAsnAsp-----IleGlyGluArgIleGlyLeuSerAspGly 341
Db 1612 -----CCGCAAAATGACAAAAATGCGCAAGCTATTAA----- 1644
QY 342 ThrTyrThrLeuThrGluLeuAsn-----SerProAlaGlyTyrSer 355
Db 1645 ---TATTAGTTAAAGAGTAATGCTCAGGTGAGATACACACGAGAGATATCT 1701
QY 356 IleAlaGlu-----ProIle-----ThrPheLysVal 364
Db 1702 AAAAAGAAATGCTTAAAGTGTACTAATCTGAAAAACCAATCGAAACCAATCAAT 1761
QY 365 GluAlaGlyLysValTyrThrIleIleAspGlyLysGlnIleGluAsnProAsnLysGlu 384
Db 1762 AGTGGTGAAGAAAGTATGGAGCAGACAAAGCAATCAAGTGGTAAGACCCAGCAAAA--- 1818
QY 385 IleValGluProTyrSerValGluAlaTyrAsnAspPheGluGluPheSerValLeuThr 404
Db 1819 -----GTACGTGTAAATTTATTTGGCTTAACGGGAGAAAGTAAACCTTACAC 1866
QY 405 ThrGlnAsnTyrAlaLysPheTyr-----AlaLysAsnLysAsnGly 419
Db 1867 GTGCATCTGAAACAAACTGGAAGCAATTTAAAGACTTACCGAAGTATGATGAAGCA 1926
QY 420 SerSerGlnValTyrCysPheAsnAlaAspLeuLysSerProProAspSerGluAsp 439
Db 1927 ---AAGAAATATGATATACAGTACCGAGATCAGCTAAAGAACTACACAAAGACATC 1983
QY 440 GlyGlyLysThrMetThrProAspPheThrThrGlyGluValLysTyrThrHisIleAla 459
Db 1984 AACGGTACGACAAATACGACAAAGATATACACGATGCGCAACAGTAACAAAA 2043
QY 460 GlyArgAspLeuPheLysTyrThrValLysProArgAspThrAspProAspThrPheLeu 479
Db 2044 AATTGGGTGACAAATATATACCAAGACGAAAGCAACCACTGAATCAAAAGTTGAGTTA 2103
QY 480 LysHisIleLysValIleGlyLys----- 488
Db 2104 TATCAAGATGAAAAAGCAAGCAAGAAAAAGCGCAATATTAAATGATCTAATAACGACA 2163
QY 489 -----GlyTyrArgGlyLysGlyAlaIleGlyTyrSerGlyLeu 502
Db 2164 CATACGTGACAGAGATTAGATGAAGAAAAAGCAAGCAAGTAATATACAGAGTCAG 2223
QY 503 ThrGluThrGlnLeuArgAlaAlaThrGln----- 512
Db 2224 GAATTAACAAGGTCAAAGGTTATATACACACATGTGATTAACATGATATGGTAACCTG 2283
QY 513 ---LeuAlaIleTyrTyrPheThrAspSerAlaGluLeuAspLysAspLysLeuLysAsp 531

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Db 2284 ATTGTCAGAAATTAATATACGCCAGAAACAAATCAATTAAGTGTGAAAAAGTATGGAC 2343
QY 532 TyrHisGlyPheGlyAspMetLysAspSerThrLeuAlaValAlaIleLeuValGlu 551
Db 2344 -----GACAAAGCAAT----- 2355
QY 552 TyrAlaGlnAspSerAsnProProGlnLeuThrAspLeuAspPheIleProAsnAsn 571
Db 2356 -----CAAGATGTATAGACAGACCAAGAAAAAGCACTGCAAT---TTATGGCTGATGA 2406
QY 572 AsnLysTyrGlnSerLeu-----IleGlyThrGlnTyrPheProGlnAspLeuVal 588
Db 2407 GAGAAAGTAAAAACGTTAGACGTGACATCTGAACAACTGGAAGTACGAA---TTTAA 2463
QY 589 AspIleIleArgMetGlnAspLysLysGluValIleProValThrHisAsnLeuThrLeu 608
Db 2464 GACTTACCGAAGTATGATGAGAAAGAAATA----- 2496
QY 609 ArgLysThrValThrGlyLeuAlaGlyLysPargThrLysAspPheHisPheGluIle--- 627
Db 2497 GAATATACAGTACGAC-----GAAGTACGTTAAAGACTACACACACATCTAAC 2547
QY 627 ----- 627
Db 2548 GSTAGACAAATACGACAAAGTATACACAGAGAGACATGCGCAACAGTAACAAAAAT 2607
QY 628 ---GluLeuLysAsnAsnLysGlnIleLeuLeuSerGlnThrValLysThrAspLysThr 646
Db 2608 TGGGATGACAAATTAATACCAAGACGCAAGCAAGCAAGCAAGCAAGTTCAGTTA--- 2664
QY 647 AsnLeuGluPheLysAspGlyLysAlaThr-----IleAsnLeuLysHis 661
Db 2665 -----TATCAAGATGAGAAAGCAAGCAAGCAAGCAAGCAAGCAATATTAAATCTAAT 2715
QY 662 GlyLysSerLeuThrLeuGlnGlyLeuProGlu-----GlyTyrSerTyr 676
Db 2716 AACTGCACACATACCTGAGACAGATTTAGTAAAGCAAAAGCAACCAAGTAAATATAC 2775
QY 677 LeuValLysGlu---ThrAspSerGluGlyTyrLysValLysValAsnSerGlnGluVal 695
Db 2776 ACAGTCGAGCAATTAACCAAGGTCAAAGCTTATACACACATGTGATTAACATGATGTG 2835
QY 696 AlaAsnAlaThrValSerLys-----ThrGlyIleThrSerAspGlu 709
Db 2836 GGCACCTGATTGTATACCAATTAATATATGCCAGAAACAACTCATATTAGTGGTAAATA 2895
QY 710 ThrLeuAlaPheGluAsnAsnLysGluProValValProThrGlyValAspGlnLysIle 729
Db 2896 GTATGGAGACGACAAAGCAATCAAGATGTAAAGACACGAAAGTCAAGTGAATTTA 2955
QY 730 -----AsnGly 731
Db 2956 TTGGCTAACGGA 2967

RESULT 9
US-09-815-242-4843
; Sequence 4843, Application US/09815242
; Patent No. US20020061569A1
GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlssen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078

```



```

NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB369
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 164:
SEQUENCE CHARACTERISTICS:
LENGTH: 27360 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 164:
US-09-070-927A-164

Alignment Scores:
Score: 0.00569 Length: 27360
Percent Similarity: 149.00 Matches: 181
Best Local Similarity: 32.02% Conservative: 120
Query Match: 19.26% Mismatches: 320
Indels: 320
Gaps: 45

US-09-494-297-2 (1-757) x US-09-070-927A-164 (1-27360)
QY 19 LeuSerLysAsnSerLysArgPheThrValThrLeuValGlyValPheLeuMetIlePhe 38
Db 12224 CTGAAGAAACAGCAGTCATGATGACGACCTATTTAGCAGCGCCCATTTCCAAATTTGG 12283
QY 39 AlaLeuValThrSerMetVal-----GlyAlaLysThr 49
Db 12284 GACCAAGCTAAACACAGCTCCTACGTAGCTACAGTAGATGCCACCGGGGTTATACCA 12343
QY 50 ValPheGly-----LeuValGlySerSerThrProAsnAlaIle 62
Db 12344 TTGGTGGGTTGCCACAGGCAATACATTTTGGGAGACAAAGCACCA----- 12394
QY 63 AsnProAspSerSerSerGluTyrArgTyrPtyrGlyTyrGlySerTyrValArgGlyHis 82
Db 12395 -----GAAAGCTATACAGTTTCGGAC 12415
QY 83 ProTyrTyrLysGlnPheArgValAlaHisAspLeuArgValAsnLeuGlyLysArg 102
Db 12416 GAATAGCTAAAGCCGAGTCATCTATGATGAAGAAACTTCAGCCGAGGAGACACA 12475
QY 103 SerTyrGlnValTyrCysPheAsnLeuLysLysAlaPheProLeuGlySerAspSer 122
Db 12476 CCA--ACCATTATTTAAACAGATGTCATTAAGATTATTTAGAAAAATGGATGAGAAG 12532
QY 123 ValLysLysTrp-----TyrLysLysHisAspGlyIleSerThrLysPhe--- 137
Db 12533 GGTAAAAAGTTAGCATGCTCGCTTTAAATTAGAGCATGCCGTACCAACCCGTTTACT 12592
QY 138 -----GluAspTyrAlaMetSerProArgIleThrGlyAspGluLeuAsnGlnLysLeu 155
Db 12593 CATGGGAGAAAGTTCCCTTGGCCCGGATGCAAC----- 12658
QY 156 ArgAlaValMetTyrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGlu-----Gly 173
Db 12629 -----AACCGAATGGCCAGTTCAGAGTGAGTACT 12658
QY 174 LeuGluPro-----LeuAsnAlaIleArgValThrGlnGluAlaValTyrTyrSerAsp 192
Db 12659 TTTAAACCGAGGCTTTATCATGTCACAGAAATCGAAGACCGCAGGCTATCTTTTAAAC 12718
QY 193 AsnAlaPro----- 195
Db 12719 ACGACCCCAACAGATTCATGTCAGACAAATACGACCGCAGCAATTCGTGATGTTTAT 12778
QY 196 -----IleSerAsnProAspGluSerPheLysArgGluSerGluSerAsn 210
Db 12779 GTCAAAATGCTTAATTACCAAGTTCTGCTGACACTAATTAATAAAGACCAAGCAGCAAT 12838

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QY 211 LeuValSerThrSerGlnLeuSerLeuMet-----ArgGlnAlaLeuLysGln--- 226
Db 12839 CCATTAGCAGGTGCGGAATTTTCACTCTTACACACAGGACCAAGCAAGCTTCGAGAACAC 12898
QY 227 ---LeuIleAspProAsnLeuAlaThrLysMetProLysGlnValProAspAspPheGln 245
Db 12899 TTAGTTTCGATGCAACGAAAGTACACTGACAGTATTAAGCCCGAGAAATATATCA 12958
QY 246 LeuSerIlePheGluSerGluAspLysGlyLysPylTyrAsnLysGlyTyrGlnAsnLeu 265
Db 12959 TTT-----GTGGAACCAAGACGCCA----- 12979
QY 266 LeuSerGlyGlyLeuValProThrLysProProThrProGlyAspProPheProPro 285
Db 12980 ---GCAGGTACCTTTTAAACATGACCAAGTGCTTCAGAGTTGCAAGGAGATCG 13036
QY 286 AsnGlnProGlnThr-----ThSerVal 293
Db 13037 GCGAAACCCAGACAGATTATAGCAACGGCTAATTTGTTAACTATCAAGCAGCGCTTAA 13096
QY 294 LeuIleArgLysTyrAlaIleGlyAspTyrSerLysLeuGlnGlyAlaThrLeuGln 313
Db 13097 TTAATCAAAAAGATGCAATGCA-----CACTTATTAAGTGTGCGACATTTTAA 13147
QY 314 LeuThrGlyAspAsnValAsnSerPheGlnAlaArgValPheSerSerAsnAspIleGly 333
Db 13148 GTGCTTGATGGCAAGGAGAAACGATTAACACAGCTTG---ACGACAAATATATCAAGG 13204
QY 334 GluArgIle-----GluLeuSerAspGlyTyrTyrThrLeuThrGluLeuAsnSerPro 351
Db 13205 GAAATGTGTGACAGACACTTACGCCCAAGAAATATCTCTTGTATGAACCAACCAAGCGCA 13264
QY 352 AlaGlyTyrSerIle---AlaGluProIleThrPheLysVal-----GluAlaLys 367
Db 13265 ACAGGCTATTTATTAATATACACAGCCAGTCCATTGAAATTCCTGAGAAAAAATGCTGT 13324
QY 368 Lys-----ValTyrThrIle 372
Db 13325 AAACAGCGGTCGTGCTGATGACAACTTTGAGATTACAAAGGCGCTTCCAAATC 13384
QY 373 IleAspGlyLysGlnIleGluAsnPro----- 381
Db 13385 GTGAAGAACGATATAGCGACACCAACCATTAACAGGTGCTGTTTGAATTTATGATCAC 13444
QY 382 AsnLysGluIleValGluProTyrSerValGluAlaTyrAsnAspPheGlnGluPheSer 401
Db 13445 AATAAACA-ATCATTAGGATTAACAGC-----AACGAGTGGCAAGATG--- 13488
QY 402 ValLeuThrThrGlnAsnTyr-----AlaLysPhe-TyrTyrAlaLysAs 416
Db 13489 -----CAAAATTATCTTAGAGACTTGGCGCAGGTACCTATTTATCAAAAGA 13536
QY 416 n-----LysAsnGlySerSerGlnValValTyrCys----- 426
Db 13537 AATCAAGCACCAAAATTATACAGATGGCGAGATTATATTTATCTGTAATTAGTAAA 13596
QY 427 -----PheAsnAlaAspLeuLysSerProProAspSerLysLysGlyLysThrMe 444
Db 13597 AGTAGAAATTCGTGTGATTTCAAAAGTATCCGAGATTT----- 13636
QY 444 tThrProAspPheThrThrGlyGluValLysTyrThrHisIleAlaGlyArgAspLeuPh 464
Db 13637 -----TTCCATATAGG-----GCCCTGCCCAATTTCAAGAGACCGCGCTTT 13680
QY 464 eLysTyrThrValLysProArgAspThrAspProAspThrPheLeuLysHisIleLysLys 484
Db 13681 TAAGAAATTCATGCGCATGGGAACCCACTTCAGAGACAGATTTTAATATGATACGA-- 13738
QY 484 sValIleGluLysGlyTyrArg-----GluLysGlyGlnAl 496
Db 13739 ---ATCGAAACCGGCAAAAATCTTTGAAAGAGAAAGTAACTGCTGAAAAGATGCTTC 13794
QY 496 allele-----GluTyrSerGlyLeuThrGlnThrGln 506

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QY 347 -----GlutEuaSnsrProAlaGly-----TyrSerIleAlaGluProIle 360  
Db 3424 AGTGAATGGCATTAATTTGATGTGCTCAATTAACCTTAATAAGCACTATCCGTCAGTG 3483  
QY 361 ThrPheLysValGluAlaGlyLysValTyrThIle---IleAspGlyLysGluIleGlu 379  
Db 3484 AATATATATA-----TCGCCCTGATCTGCTGCTGTTGGAGAAAAGAGATCACC 3534  
QY 380 AsnProAsnLysGluIleValGluProTyrSerValGluAlaTyrAsnAspPheGlu--- 398  
Db 3535 AAACAGACAGAAATAGTAAGATGGCTATCAAACTGAACGGATTATGTAACCTA 3594  
QY 398 ----- 398  
Db 3595 AATGGCGCATTCGCTATGATGGCACTGGATACGCCATCACTTGTGATCAAT 3654  
QY 399 ---GluPheSerValLeuThrThrGluAsn-----TyrAlaLysPhe 411  
Db 3655 AAAAATATATCCGCTAAAACTGAAATAAGAGCGCCGCACTCTATGTGCGGT 3714  
QY 412 TyrTyrAlaLysAsn----- 416  
Db 3715 TATCAAGGTGAATATCGTTCCTGCTGATGTTTATTAACCAACAGACACACTAGTACT 3774  
QY 417 ---LysAsnGlySerSerGlnValValTyrCysPheAsnAlaAspLeuLysSerPro 435  
Db 3775 TATATAAACGCTTCATGACAGATATATATCTTT---GCTGATATGGCATCC----- 3825  
QY 436 AspSerGluAspGlyLysThrMetThrPro----- 446  
Db 3826 -----AAAGATATGACCCCGAAGACAGCAATGTATTATCGGATAAAT 3867  
QY 446 ----- 446  
Db 3868 AGCTATCAACAATTTATACCAATATATGCAGAGAGTGAATACCGCTATGCAGAGAT 3927  
QY 447 -----AspPheThrThrGlyGluValLysTyr 455  
Db 3928 TATGAGATTCCTTCCTCGGTAAGTACCGTAAGACTATGGTGGGAGATTATTACCTC 3987  
QY 456 ThrHisIleAlaGlyArgAspLeuPheLysTyrThrValLysProArgAspThrAspPro 475  
Db 3988 AGCATGTATATTAACGAGATATATCCAACTATCAATTAACAAACCCGATCACTGATTTA 4047  
QY 476 AspThrPheLeuLysHisIleLysValIleGluLysGlyTyr-----Arg 491  
Db 4048 AAAATCTATATCCACCAAAATTAAGAATATTATCAATATGATATAGAGACAGAAAGCCG 4107  
QY 492 GlnLysGlyLysAlaIleGluTyrSerGlyLeuThrGluThrGlnLeuArgAlaIleThr 511  
Db 4108 AATCAATGCAATCTGATGAATAAATATGCAAACTAGTGATTAATTTATTGTTATATCT 4167  
QY 512 GlnLeuAlaIleTyrTyrPheThrAspSerAlaGluLeuAspLysAspLysLeuLysAsp 531  
Db 4168 ACCTGGGGGTCATCAATAATATCTGCAAAATATACCTCATGTTTACCCGCTATCAAA 4227  
QY 532 TyrHisGlyPheGlyAspMetAsnAspSerThrLeuAlaValAlaLysIleLeuValGlu 551  
Db 4228 TATAGGGA-----AACACCATGGACTCAATCAAGGAGACTACTA----- 4269  
QY 552 TyrAlaGlnAspSerAsnProProGlnLeuThrAspLeuAspPhePheIleProAsnAsn 571  
Db 4270 TTCACCGCTGACACCACTTATCA-----TCTAAAGTAGAACCTTGATTCCTGAGCA 4323  
QY 572 AsnLys-----TyrGlnSerLeuIleGlyThrGlnTyr----- 582  
Db 4324 AAACGTTCTTAACAACAATAATGCCGCGGATGGATGATTAATCTACAGACTCTG 4383  
QY 583 ---HisProGlnAspLeuValAspIleIleArgMetGluAspLysGluValIle----- 600  
Db 4384 AATAAACCGGATGATTTAAGCAATATATCTTTATATACGACGTAAGAGGACTGCTACT 4443  
QY 601 -----ProValThrHisAsnLeuThrLeu-----ArgLysThrValThr 613

Db 4444 GATGTCACAGCCGAGTAGAGATTAAATGATTCGCAATTTCTCCAGCAAAAGTTCAAGATATA 4503  
QY 614 GlnLeuAlaGlyAspArgThrLysAspPheHisPheGlu----- 626  
Db 4504 GTCAAAGCGGCTGCAAGGAGCAAACTTTTACCGCAGATGAAGATGTCCTCATCAGCCA 4563  
QY 627 -----IleGluLeuLysAsnAsnLys 633  
Db 4564 TCACCTAGCTTTATGAAATGAATTTATCAATTTAAATGCCCTTAATAAGCGTTCTGGT 4623  
QY 634 GlnGluLeuLeuSerGlnThrValLysThrAspLysThrAsnLeuGluPhe---LysAsp 652  
Db 4624 CTGAATTTTATTAACAACCTGACGAGATGATGATGATTTTACCGCATTTGGCGAGAT 4683  
QY 653 GlyLys-----AlaThrIleAsnLeuLysHisGly 662  
Db 4684 GGCCGCAAACTGGGTTATGAACCTTCAGTATTCCTGTTACCTCAAGGTAAAGTACCGAT 4743  
QY 663 GluSerLeuThrLeuGlnGlyLeuProGluGlyTyrSerTyrLeuValLysGluThrAsp 682  
Db 4744 AATGCCCTGACCTGCAACCTAATGAATAATGTGCGCATATATG-----CAA 4791  
QY 683 SerGluGlyTyrLysValLysValAsnSer-----GlnGluValAlaAsnAla 698  
Db 4792 TGCAATTCCTATGATCCGCGCTGAATACTATTTGCCGCGCATGTTGGTGCAGCGCC 4851  
QY 699 ThrValSerLysThrGlyIleThrSerAspGluThrLeuAlaPheGluAsnAsnLysGlu 718  
Db 4852 ACC-----ACCGAATCGATCAATTCGTAGATGGAACCTAGAAATATTCAGGAA 4902  
QY 719 ProValValProThrGlyValAspGlnLysIleAsnGlyTyrThrLeuAlaLeuIleValIle 738  
Db 4903 CCG-----CAGTTAAGCAAAAGTTTCTATGCTACGTTCTGATTA 4941  
QY 739 AlaGlyLysSerLeuGlyIleTyrGly 747  
Db 4942 CTCCTCATTAACCTATCACTCATGCT 4968

RESULT 7  
US-09-070-927A-164  
Sequence 164, Application US/09070927A  
Patent No. US20020120116A1  
GENERAL INFORMATION:  
APPLICANT: Charles A. Kunsch  
Steven Barash  
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides  
NUMBER OF SEQUENCES: 982  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/070,927A  
FILING DATE: 04-May-2000  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/046,655  
FILING DATE: 1997-05-16  
APPLICATION NUMBER: 60/044,031  
FILING DATE: 1997-05-06  
APPLICATION NUMBER: 60/066,009  
FILING DATE: 1997-11-14  
ATTORNEY/AGENT INFORMATION:

```

OY      683  SerGluGlyTYRLeuValAlaAsn-----GlnGluValAlaAsnIle 698
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Db      4792  TGGCAATCTTTCGTACCCGCCCTGAATACTATTTCGCCCGCAGTTGGTGACGCACC 4855
          :|||:::  :::|||||:::  :::  :::  :::
OY      699  ThrValSerLysrHngLyIleTherSexAspGluThrLeuAlaPheGluAsnAsnLysGlu 718
          |||  |||||:::  :::  :::  :::  :::
Db      4852  ACC-----ACCGAATCGATAACAATTCTGTGATGAAACCAACAATATTTCAGGAA 4905
          :|||  |||||:::  :::  :::  :::  :::
OY      719  ProValProHrnHngLyValAlaSpGlnLysIleAsnGlyTYRLeuAlaIleuIleValIle 738
          |||  |||  |||||:::  :::  |||  |||||
Db      4903  CCG-----CAGTTAGCAAGAAGGTTCTATGTAAGTCTGATGATGATGATGATGATGAT 4941
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OY      739  AlaGlyIleSerLeuGlyIleTyrgly 747
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Db      4942  CCTCCCTAATACCTATCATCATGTGT 4968
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RESULT 6
US-10-242-056-46
Sequence 46, Application US/10242056
Publication No. US20030113323M1
GENERAL INFORMATION:
APPLICANT: Ensign, Jerald C
APPLICANT: Bowen, David J
APPLICANT: Petell, James
APPLICANT: Fatig, Raymond
APPLICANT: Schoonover, Sue
APPLICANT: French-Constant, Richard
APPLICANT: Orr, Gregory L
APPLICANT: Merlo, Donald J
APPLICANT: Roberts, Jean L
APPLICANT: Rochelleau, Thomas A
TITLE OF INVENTION: Insecticidal Protein Toxins from
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dowelanco
STREET: 9330 Zionsville Road
CITY: Indianapolis
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/242,056
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/063,615
FILING DATE: 18-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/395,497
FILING DATE: 28-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/007,255
FILING DATE: 06-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/608,423
FILING DATE: 28-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/705,484
FILING DATE: 28-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/743,699
FILING DATE: 06-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Borucki, Andrea T.
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 50301E
TELECOMMUNICATION INFORMATION:

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[illegible]



Db 2650 GCACAAACATGTAATGCCGCCACAGGCGTTTCGGCTTGGTCC--GGGCGGATTAAT 2706  
Oy 177 LeuAsnAlaIleArgValThrGlnGlu---AlaValTrpTyrTyrSerAsp-----192  
Db 2707 ATTCATTCATGAAAGAGACAGCAGCTATGCCAGTGGGAGAAAACGGGAGCGGTATTA 2766  
Oy 193 -----AsnAlaProIleSerAsnProAspGluSerPheLysArgGluSerGlu 208  
Db 2767 ACCGCGGCGTTGAATTCACACAGCGTAATACATTCACACGCTTTCTCGATGTAATCGCG 2826  
Oy 209 SerAsnLeuValSerThr-----SerGlnLeuSerIleuMetArgGlnAlaLeuLys 225  
Db 2827 AGTGGCGCATTAAGACCTACTATATCCGTAAGTCGCAAGCAGCGCGGCTATTAA 2886  
Oy 226 Gln-----LeuIleAspProAsnLeuAla-----233  
Db 2887 AGCGCGATGACTTGTATCAATACTTACTGATTTGATTAATAGCTTTCGCGCAATATAA 2946  
Oy 234 ---ThrLysMetProLysGlnValProAspAspPheGlnLeu-----246  
Db 2947 ACCACCGGATCGCCGAGGCAAGCATTTGCC---AGTATTCAACTGTACGTCAACCGGCGATTG 3003  
Oy 247 ---SerIlePheGlnSerGluAspLysGly-----255  
Db 3004 GAAATAGTGGAAGAAATGCGCAATTCGCGGGTATACAGCCGCCAATTCCTTATCGACTGG 3063  
Oy 256 AspLysTyrAsnLysGlyTyrGlnAsnLeuSerGlyLysLeuValProThrLysPro 275  
Db 3064 GACAAATACATTAATACGCTACACACTTGGCGGGGTTCCTCAATTAGTTTACTACCG 3123  
Oy 276 ProThrProGlyAspProPheMetProProAsnGlnProGlnThrThrSerValLeuIle 295  
Db 3124 GAAACTATATGTATCGACCATCGATCGATCGACAAACCAAAATGATGACGCAATTACTG 3183  
Oy 296 ArgLysTyrAla-----299  
Db 3184 CAATCCGTCAGCAAAACCAATTAACGCCGATACCGTCGAGATGCGCTTATGCTTAT 3243  
Oy 300 IleGlyAspTyrSerLysLeuGlnGluGlyAlaThrIleuGlnLeuThrLysAspAsnVal 319  
Db 3244 CTACACATCGTTTACAAACAGTGGCTAATCTTAAAGTATTATGCGCATATACGATTAATAT 3303  
Oy 320 AsnSerPheGlnAlaArgValPhe-----SerSerAsnAspIleGlyLys---334  
Db 3304 AATAAGCATCAAGCGCTACACTTATTTATCGACTAGTGAACGTATGCCGGTGAAATAT 3363  
Oy 335 -----ArgIleGlnLeuSerAspGlyThrTyrThrIleuThr-----346  
Db 3364 TATTTGGCGAGTGTGATCACAGTAAATTCACAGCGTAAATTCGCGGCTAATGCGCTGG 3423  
Oy 347 -----GluLeuAsnSerProIleGly-----TyrSerIleAlaGluProIle 360  
Db 3424 AGTGAAATGGCATAAATTTGATTTGCCAATTAACCTTATTAAGACACTATCCGTCAGTG 3483  
Oy 361 ThrPheLysValGlnAlaGlyLysValTyrThrIle---IleAspLysGlnIleGlu 379  
Db 3484 ATATATATAA-----TCCCGCTGTATCTGCTGTGGTGAACAAAGAGATCACC 3534  
Oy 380 AsnProAsnLysGlnLeuValGluProTyrSerValGlnAlaTyrAsnAspPheGlu---398  
Db 3535 AAACACACAGGAATAGTAAAGATGCTTCAACAACTGAACGAGTATTCGTTATGAACCTA 3594  
Oy 398 -----398  
Db 3595 AAATTTGGCGATATCCGCTATGATGGCACTTGAATACGCCAATCACTTATGTCAT 3654  
Oy 399 ---GluPheSerValLeuThrThrGlnAsn-----TyrAlaLysPhe 411  
Db 3655 AAAAAATATTCGAGCTAAACCTGAGAAAAAATAGAGCGCCGAGCTATATGTGCGGCT 3714  
Oy 412 TTTTAT 416  
Db 3715 TATCAAGAGTGAATACGTTGCTGTGATGTTTATTAACCAACAGACACATAGATAGT 3774

Oy 417 ---LysAsnGlySerSerGlnValValTyrCysPheAsnAlaAspLeuLysSerProPro 435  
Db 3775 TATATAAAACCGCTTCATACAGAGCATATATATCTTT---GCTGATATAGCATCC-----3825  
Oy 436 AspSerGluAspGlyLysThrMetThrPro-----446  
Db 3826 -----AAAGATATGACCCAGAACAGACGCAATGTTTATCGGATTAAT 3867  
Oy 446 -----446  
Db 3868 AGCTATACAAATTTGATACCAATATATGTCAGAGAGTGAATAACGCTATGACAGAGAT 3927  
Oy 447 -----AspPheThrThrGlyGlnValLysTyr 455  
Db 3928 TATGAGATTCCTTCCTCGTAACTAGCCGTAAGACACTATGTTGGGAGATTATTAACCTC 3987  
Oy 456 ThrHisIleAlaGlyArgAspLeuPheLysTyrThrValLysProArgAspThrAspPro 475  
Db 3988 AGCATGGTATATACGAGATATATCCAACTATCAATTAACAAGCCGATCAAGTATTA 4047  
Oy 476 AspThrPheLeuLysHisIleLysValIleGluLysGlyLys-----Arg 491  
Db 4048 AAATCTATATCTACCCAAATTAAGATTAATTAATGATATGAAGAGACAGAACCGC 4107  
Oy 492 GlnLysGlyGlnAlaIleGlyTyrSerGlyLeuThrGlnLeuArgAlaAlaThr 511  
Db 4108 AATCAATGCAATCTGATGATTAATATGGAACACTAGTATTAATTTATGTTTATACT 4167  
Oy 512 GlnLeuAlaIleTyrTyrPheThrAspSerAlaGlnLeuAspLysAspLysLysAsp 531  
Db 4168 AGCTTGGGGTCAATCCAAATTAACCTGCTCAATATAGCTATGTTTACCCGCTATCA 4227  
Oy 532 TyrHisGlyPheGlyAspMetAsnAspSerThrLeuAlaValAlaLysIleLeuValGlu 551  
Db 4228 TATAGCGGA-----AACCCAGTGAAGTCAATCAAGAGACACTATA-----4269  
Oy 552 TyrAlaGlnAspSerAsnProProGlnLeuThrAspLeuAspPheIleProAsnAsn 571  
Db 4270 TTCACCGGTACACCACTTATCCA-----TCTAAAGTAAAGACTTGATCTCTGGAGCA 4323  
Oy 572 AsnLys-----TyrGlnSerLeuIleGlyThrGlnTrp-----582  
Db 4324 AAACGCTCTTAACCAACCAAAATGCCGCAATGGTATGATATGATACAGACTGCTG 4383  
Oy 583 ---HisProLysPheLeuValAspIleIleArgMetGlnAspLysGluValIle---600  
Db 4384 AATTAACCGGATGATCTTAAGCAATATATCTTATGACTGACAGTAAAGGAGCTGTA 4443  
Oy 601 -----ProValThrHisAsnLeuThrLeu-----ArgLysThrValThr 613  
Db 4444 GATGTCACAGGCCAGTAAAGATTAATACAGCAATTTCTCCACAAAAGTTCAGATATA 4503  
Oy 614 GlyLeuAlaGlyAspArgThrLysAspPheHisPheGlu-----626  
Db 4504 GTCAAGCGGGTGGCAAGAGCAAACTTTAACCGAGATTAAGATGCTCATTCAGCCA 4563  
Oy 627 -----IleGlnLeuLysAsnAsnLys 633  
Db 4564 TCACCTAGCTTGTATGAATGAATTAATCAATTAATGCCCTTGAATATACGCGTTCTGGT 4623  
Oy 634 GlnGluLeuLeuSerGlnThrValLysThrAspLysThrAsnLeuGluPhe---LysAsp 652  
Db 4624 CTGAATTTATTAACAACCTAGCAGATATGATGATTTTACCGCATTTTGGGAGAGAT 4683  
Oy 653 GlyLys-----AlaThrIleAsnLeuLysHisGly 662  
Db 4684 GGCCGCAAACTGGGTTATGAAGCTTTCAGATATCTGTTTACCTCAAGGATTAATACGAT 4743  
Oy 663 GluSerLeuThrLeuGlnGlyLeuProGlnGlyTyrSerTyrLeuValLysGluThrAsp 682  
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Db 3160 ACTGAATGGCAATAAATGATGTGCAATTAACCTTATAAAGACATATCCGTCACAGTG 3219
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Qy 361 ThrPheIysValGluAlaGlyValIleThrTle---IleAspGlyLeuGlu 379
      ::::::::::: |||
Db 3220 ATATATATAA-----TCCCGCTGTATCTGCTGTGTGAGCAAAAGAGATCCACC 3270
      ::::::::::: |||
Qy 380 AsnProAsnIysGluIleValGluProIysSerValGluAlaIleTyrAsnAspHeGu--- 398
      ::::::::::: |||
Db 3271 AAACAGACAGCAAAATAGTAAGATGCTATCAAACTGAAAGCAGATTATCTTATGACTA 3330
      ::::::::::: |||
Qy 398 ----- 398
Db 3331 AAATGGCGCATATCCGCTATGATGCACTTGGAATAGCCCAATCACCCTTGATGTCAAT 3390
      ::::::::::: |||
Qy 399 ---GluPheSerValLeuThrGlnAsn-----TyrAlaIysPhe 411
      ::::::::::: |||
Db 3391 AAAAAAATATCCGACTAAACCTGAAAAAATAGACGCCGCCGACTCTATTTGTCGGGT 3450
      ::::::::::: |||
Qy 412 TyrTyrAlaIysAsn----- 416
      ::::::::::: |||
Db 3451 TATCAAGGTGAAGATACGTTGCTGATGTTTATACCAACAAAGACACTAGATAGT 3510
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Qy 417 ---LysAsnGlySerSerGlnValValIleTyrCysPheAsnAlaAspLeuIysSerPro 435
      ::::::::::: |||
Db 3511 TATAAAACGCTTCATGCAAGACTATATATCTTT---GCTGATATGCGATCC----- 3561
      ::::::::::: |||
Qy 436 AspSerGluAspGlyGlyIysThrMetThrPro----- 446
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Db 3562 -----AAAGATATGACCCCAAGACAGCAATGTTTATGCGGATAT 3603
      ::::::::::: |||
Qy 446 ----- 446
Db 3604 AGCTATCAACATTTGATACCAATATGTCAGAAAGTCATACCCGCTATGCAGAGAT 3663
      ::::::::::: |||
Qy 447 -----AspPheThrGlyGluValIysTyr 455
      ::::::::::: |||
Db 3664 TATGAGATTCCTTCTCGGTAGTAGCCGTAAGACTATGTTGGGAGATATTATACCTC 3723
      ::::::::::: |||
Qy 456 ThrHisIleAlaGlyArgAspLeuHeIysTyrThrValIysProArgAspThrAspPro 475
      ::::::::::: |||
Db 3724 AGCATGTATATACGAGATATTTCCAACTATCAATTCACAAAGCCGATCAAGTATTTA 3783
      ::::::::::: |||
Qy 476 AspThrPheLeuIysHisIleIysIysValIleGluIysGlyTyr-----Arg 491
      ::::::::::: |||
Db 3784 AAAATCTATATCTCCACAAATTAAGATATTATTCATATGATATGAAGAGACAGAACCC 3843
      ::::::::::: |||
Qy 492 GluIysGlyGlnAlaIleGluTyrSerGlyLeuThrGluThrGlnLeuArgAlaIleThr 511
      ::::::::::: |||
Db 3844 AATCAATGCATCTGATCAATTAATATGCAAACTAGCGATAAATTTATGTTATATCT 3903
      ::::::::::: |||
Qy 512 GlnLeuAlaIleTyrThrPheThrAspSerAlaGluLeuAspIysAspIysLeuAsp 531
      ::::::::::: |||
Db 3904 AGCTTGGGGGTCAATTCACAAATACCTGTCAAATGCTCATGTTTATCCCGCTATCA 3963
      ::::::::::: |||
Qy 532 TyrHisGlyPheGlyAspMetAsnAspSerThrLeuAlaValAlaIysIleLeuValGlu 551
      ::::::::::: |||
Db 3964 TATAGCGGA-----AACACAGTGAGCATCAATCAAGGAGATCTA----- 4005
      ::::::::::: |||
Qy 552 TyrAlaGlnAspSerAsnProProGlnLeuThrAspLeuAspPhePheIleProAsnAsn 571
      ::::::::::: |||
Db 4006 TTCCACCGGTGACACACTTATCCA-----TCTAAGTAGAAGCTTGATCTCTGAGACA 4059
      ::::::::::: |||
Qy 572 AsnIys-----TyrGlnSerLeuIleGlyThrGlnIleTyr----- 582
      ::::::::::: |||
Db 4060 AAACGTTCTCTTACCAACCAAAATGCGCATGTTGATGATTAATGATACAGACACTCTCTG 4119
      ::::::::::: |||
Qy 583 ---HisProGluAspLeuValAspIleIleArgMetGluAspIysGluValIle--- 600
      ::::::::::: |||
Db 4120 AATAAACCGGATGATTAAGCAATATATCTTATGACTGACAGATAAAGGAGCTCTACT 4179
      ::::::::::: |||
Qy 601 -----ProValThrHisAsnLeuThrIleu-----ArgIysThrValThr 613
      ::::::::::: |||

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Db 4180 GATGCTCAGCCAGTAGATGATTAATCTGCAATTTCTCAGCAAAAGTTCAGATTAATA 4239
      ::::::::::: |||
Qy 614 GlyLeuAlaGlyAspArgThrIysAspPheHisPheGlu----- 626
      ::::::::::: |||
Db 4240 GTCAAAAGCGGGGACAGAGAGCAAACTTTACCGAGATAAAGATGTCTCATGACCA 4299
      ::::::::::: |||
Qy 627 -----IleGluLeuIysAsnIys 633
      ::::::::::: |||
Db 4300 TCACCTAGCTTGATGAATGAATATATCAATTTATGCCCTTGAAATAGACGTTCTGT 4359
      ::::::::::: |||
Qy 634 GlnGluLeuIysSerGlnThrValIysThrAspIysThrAsnLeuGluPhe---LysAsp 652
      ::::::::::: |||
Db 4360 CTGAATTTTATTAACAACTACACAGCAGTATGATGTTACTTTTACCGCATTTGCGAGAT 4419
      ::::::::::: |||
Qy 653 GlyIys-----AlaThrIleAsnLeuIysHisGly 662
      ::::::::::: |||
Db 4420 GCCCCCAAACTGGTTATGAAGTTTCAGTATTCCTGTTTACCTCAAGTAAGTACCGAT 4479
      ::::::::::: |||
Qy 663 GluSerLeuThrLeuGlnGlyLeuProGluGlyIysTyrSerTyrLeuValIysGluThrAsp 682
      ::::::::::: |||
Db 4480 AATGCCCTGACCTGCACCATATATGAATGATGTCGCGCATATATG-----CA 4527
      ::::::::::: |||
Qy 683 SerGluGlyTyrIysValIysValAsnSer-----GlnGluValAlaAsnAla 698
      ::::::::::: |||
Db 4528 TGGCAATCCTATGTAACCGCTGAACTATTTGCCCCGACAGTGTGTCACAGCGCC 4587
      ::::::::::: |||
Qy 699 ThrValSerIysThrGlyIleThrSerAspGluThrIleAlaPheGluAsnAsnIysGlu 718
      ::::::::::: |||
Db 4588 ACC-----ACCGGAATCGATACAAATTCGATGATGAGAACTGAGAAATTTTCAGGA 4638
      ::::::::::: |||
Qy 719 ProValIleProThrGlyValAspGlnIysIleAsnGlyTyrLeuAlaIleValIle 738
      ::::::::::: |||
Db 4639 CCG-----CAGTTAGCAAAAGTTTCTATGCTACGTCGTGATA 4677
      ::::::::::: |||
Qy 739 AlaGlyIleSerLeuGlyIleTyrGly 747
      ::::::::::: |||
Db 4678 CCTCCCTAATACCTATCAACTCATGTGT 4704
      ::::::::::: |||

RESULT 5
US-09-817-514A-1
; Sequence 1, Application US/09817514A
; Patent No. US20020078478A1
; GENERAL INFORMATION:
; APPLICANT: fferench-constant, Richard
; APPLICANT: Bowen, David
; APPLICANT: Rocheleau, Thomas
; APPLICANT: Waterfield, Nicholas
; TITLE OF INVENTION: DNA SEQUENCES FROM PHOTORHABDUS LUMINESCENS
; FILE REFERENCE: 61645
; CURRENT APPLICATION NUMBER: US/09/817,514A
; CURRENT FILING DATE: 2000-03-26
; PRIOR APPLICATION NUMBER: US 60/191806
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 7551
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
; US-09-817-514A-1

Alignment Scores:
Pred. No.: 0.000435 Length: 7551
Score: 152.00 Matches: 148
Percent Similarity: 33.13% Conservative: 120
Best Local Similarity: 18.29% Mismatches: 287
Query Match: 3.85% Indels: 254
DB: 9 Gaps: 37

US-09-494-297-2 (1-757) x US-09-817-514A-1 (1-7551)
Qy 157 AlaValMetTyrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGluGlyLeuGluPro 176
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Db      2995  ACACAGTAC-----GACACGCGACCTGACATTGCGCATATTCCG 3036
QY      661  HlsglygluSerLeuThrLeuGln---GlyLeuProGluGlyTyrSerLeuValLys 679
Db      3037  TATGGCACTTACATTTTAAATAAATCAAGGCGCGCGGATATACG-----ATCAGC 3090
QY      680  GluThrAspSerGluGlyTyrLysValLysValAsnSerGln-----693
Db      3091  GACGCGTATGACGAGCGGGGTCTCCGTTGAGATTACAGACAGCTTCAAGTCCGCGAGCG 3150
QY      694  -----GluValAlaAsnAlaThrValSerLysThrGlyLysThrSerAspGlu 709
Db      3151  CTTTACAAAGTCGTGATGAGAAGAAATTAAGTGACGCTTATCAAAACAGACGAA 3204

RESULT 4
US-10-242-056-48
; Sequence 48, Application US/10242056
; Publication NO. US20030113323A1
; GENERAL INFORMATION:
; APPLICANT: Emisip, Jerald C
; APPLICANT: Bowen, David J
; APPLICANT: Petell, James
; APPLICANT: Facily, Raymond
; APPLICANT: Schoonover, Sue
; APPLICANT: Ifrench-Constant, Richard
; APPLICANT: Orr, Gregory L
; APPLICANT: Merlo, Donald J
; APPLICANT: Roberts, Jean L
; APPLICANT: Rocheleau, Thomas A
; TITLE OF INVENTION: Insecticidal Protein Toxins from
; TITLE OF INVENTION: Photornabidus
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dowelanco
; STREET: 9330 Zionsville Road
; CITY: Indianapolis
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/242,056
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/063,615
; FILING DATE: 18-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/395,497
; FILING DATE: 28-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/007,255
; FILING DATE: 06-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/608,423
; FILING DATE: 28-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/705,484
; FILING DATE: 28-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/743,699
; FILING DATE: 06-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Borucki, Andrea T.
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 50301E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-337-4846

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; TELEFAX: 317-337-4847
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5547 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-10-242-056-48

Alignment Scores:
Pred. No.: 0.000276
Score: 152.00
Percent Similarity: 33.13%
Best Local Similarity: 18.29%
Query Match: 3.85%
DB: 14
Gaps: 37

US-09-494-297-2 (1-757) x US-10-242-056-48 (1-5547)
QY      157  AlavalMetCyrAsnGlyHisProGluAsnAlaAsnGlyLysMetGluGlyLeuGluPro 176
Db      2386  GCACAAACAAATGATGATTCGCCCCACAGGGCGTTTCGCTTGAT 2442
QY      177  LeuAsnAlaIleArgValThrGlnGlu---AlaValIlePheTyrSerAsp-----192
Db      2443  ATTCAATCAATGAAAGAACAGACCGACCTATGCCAGTGGAAACCGCGGACGCTATTA 2502
QY      193  -----AsnAlaProIleSerAsnProAspGluSerPheLysArgGluSerGlu 208
Db      2503  ACCGCGGGTGTGAATTCACAAACAGGCTAATACATTCAGCGCTTGTGTAATCTCCG 2562
QY      209  SerAsnLeuValSerThr-----SerGluLeuSerLeuMetArgAlaLeuLys 225
Db      2563  AGTGCCGCAATTAAGCACTACTATATCCGTCAAGTCGCCAAGCAGCGCGCTATTAA 2622
QY      226  Gln-----LeuIleAspProAsnLeuAla-----233
Db      2623  AGCGGTGATGACTTGTATCAATCTTACGATTCAGTATGATATCAAGTTCTCGGCAATAAA 2682
QY      234  ---ThrLysMetProLysGlnValProAspAspPheGlnLeu-----246
Db      2683  ACCACCGGATCGCCCAACAGCATTCGCC---AGTATTCACATCTCAACCGCGCATTCG 2739
QY      247  ---SerIlePheGluSerGluAspLysGly-----255
Db      2740  GAAATATGTGAGAAAGAAATGCGAATTCGGGGGTTATAGCCGCCAATCTTTATCGACTGG 2799
QY      256  AspLysTyrAsnLysGlyTyrGlnAsnLeuLeuSerGlyGlyLeuValProThrLysPro 275
Db      2800  GACAAATACATTAAGCTACAGCACTTGGCGGGGTTCCTCAATTAAGTTACTGACCGG 2859
QY      276  ProThrProGluAspProPheMetProProAsnGlnProGluInThrThrSerValLeuIle 295
Db      2860  GAAACTATATGATTCGACCATTCGCTATCGCAACCAAAATGATGAGCAGCATTAACG 2919
QY      296  ArgLysTyrAla-----299
Db      2920  CAATCCGTGACGCAAAACCAATTAAGCGCGATACCGTGGAAGACCTTTATGCTTAT 2979
QY      300  IleGlyAspTyrSerLysLeuLeuGluGlyAlaThrLeuGlnLeuThrGlyAspAsnVal 319
Db      2980  CTGACATCGTTTGACAAATGGCTATCTTAAAGTATTAAGCCATATCAAGCATATAT 3039
QY      320  AsnSerPheGlnAlaArgValPhe-----SerSerAsnAspIleGlyGlu---334
Db      3040  AATAACGATCAAGGGCTGACCTATTTATCGCACTGAGGAACATGATCCGCTGAATAT 3099
QY      335  -----ArgIleGluLeuSerAspGlyThrTyrThrLeuThr-----346
Db      3100  TATTGCGCAGTGTGCATCACAGTAAATTCACAGAGCGTAATTCGGGCTAATGCGCTGG 3159
QY      347  -----GluLeuAsnSerProAlaGly-----TyrSerIleAlaGluProIle 360

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QY	114	AlaPheProLeuGlySerAspSerSerValIlyLysIlyrTYrTYrLYsLYsHisAspGlyIle	133
DB	985	GCTTACGCCCTCATCTATGTATGACGACGATCGATCGATCTCCGCAAAACGACAAAGCGCGCA	1044
QY	134	SerThrLYsPheGluAspTYrAlaMetSerProArgIleThrGlyAspGluLeuAsnGln	153
DB	1045	AACGCTGCATTATGACAAACAGCA-----	1068
QY	154	LysLeuArgAlaValMetTYrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGluGly	173
DB	1069	-----ACGTTCCGGCGCA-----GACAT	1086
QY	174	LeuGluProLeuAsnAla-----IleArgValThrGln	184
DB	1087	CTTGACACCGGCTTCTGACAGAGCCCTCTGTACGGCCAAATACGGGAAATGATCCAAAA	1148
QY	185	GluAlaValIlePPTyTYrSerAspAsnAlaProIleSer-----AsnPro	199
DB	1147	TGCTGCAGAGTTATTAAGAGGATTCACAGACGTTCACCTGAGCATTTTATATACAT	1206
QY	200	AspGluSerPheLYsArgGluSerGluSerAsnLeuVal-----SerThrSerGln	216
DB	1207	GGAGAGAAAAAATGACGCAATCCAAACGACGACATACAGACTGCTTGGTTCCTCAT	1266
QY	217	LeuSerLeuMetArgGlnAlaLeuLysGlnLeu-----IleAspProAsnLeuAla	233
DB	1267	TTGCATCTTGTTCAGATTCTTAAAGGTGATTCGATTTACTTTCATTCACAGACGCGCAGT	1326
QY	234	ThrLYs-----MetProLYsGlnValProAspAspPheGlnLeuSer-----	247
DB	1327	GAGCAGGCTGCAAGCCCTTAACGACGACGAGGATTTATACGCTCTTCGATTAATGCAAGC	1386
QY	248	-----IlePheGluSerGluAspLYsGlyAspLYsTYrAsnLYsGlyTYrGlnAsn	264
DB	1387	GGGTTTGAATCAATTAACCAAGATGTTACCGGAGCTTCAAAATACAGCATACAAAC	1448
QY	265	LeuLeuSerGlyGlyLeuValProThrLYsProProThrProGlyAspProPheMet--	283
DB	1447	GAGGTCAACACCGGAGTAAATCATGATTAATCAACACCTATACGACACATCGACGTGCC	1506
QY	284	-----ProProAsnGlnProGlnThrThrSerVal-----LeuIleArgLYs	297
DB	1507	GGACACGAGCAATCAAAAGAAAGCTTCAGGTACAGCCGTTCAAGCAGATTTGATTAAGGC	1566
QY	298	TYrAlaIleGlyAspTYrSerLYsLeuLeuGluGlyAlaThrLeuGlnLeuThrGlyAsp	317
DB	1567	TACTCAAAACATTGATTACMAAGAAACGGTCCGATTCGACATCGCAATC-----	1617
QY	318	AsnValAsnSerPheGlnAlaArgValPheSerSerAsnAspIleGlyGluArg-----	335
DB	1618	AACAAAAACAACTACACGATACACATTTGGAAAGTTGGATGACAAATTCGAAAGCGCGGG	1677
QY	336	IleGluLeuSerAspGlyTYrThrTYrThrLeuThrGluLeuAsnSerProAlaGlyTYrSer	355
DB	1678	CTCACGCTCTCTCGACGATCATTCGCGCTTCAGAGTGTGAGCAAT-----	1722
QY	356	IleAlaGluProIleThrPheLYsValGluAlaGlyLYsValTYrThrIleIle-----	373
DB	1723	-----AACAAACCCCTTGACAAAGGCAAAAGCTATACATTGATATATATAA	1767
QY	374	-----AspGlyLYsGlnIleGlu-----AsnProAsnLYsGlu	384
DB	1768	CCGGAATCATGAAGGTTTCTCTCGAATCATCGAGATTTATGGCAGACACAGACAGCCAG	1827
QY	385	IleValGluProTYrSerValGluAlaTYrAsnAspPheGluGluPheSerValLeuThr	404
DB	1828	CTTAAAGATCAGGTATACCAACAAATATCAATCCGCACTTTTCCAAAGAAATGTCAAAAAC	1887
QY	405	ThrGlnAsnTYrAlaLYsPheTYrTYrAla-----LysAsnLYsAsnGlySer	420
DB	1888	ACGGCAGCATACAGTGGACTGATCATCGACGACACTGAAACGCAAAAATTAAGAAACGCGAGC	1947

QY	421	Se	-----	421
Db	1948	AGTTTACGCGGAATCGCCAGACATCCCAACAGCGCTTCAACACGCGTTATACAGGCT	2007	
QY	442	-----GlnValValTyrCysPheAsnIAspLeuLysSerProProAspSerGlu	438	
Db	2008	GTTTCAAAAGAAATCAGCTGGAAAAATCGGCATCACTTAATGGAGACCGCTCAAAAAAC	2067	
QY	439	AspGIgLYLysThrMetThrProAsp-----PheThrThrGlyGluVal-----	453	
Db	2068	CCTTATATTAAAGATCTTTTAGCAGATGATCCAGCAGCATTTGAAAAAGCGTGGTGTGTGCT	2127	
QY	454	-----LysTyrThrHisIleAlaGlyArgAspLeuPhe-----	464	
Db	2128	AAGAGCTATTCAGTTAATATAAGACGGTTCATCACAGAAAGAGACATCTCCGCGCTCC	2187	
QY	465	LysTyrThrVal-----LysProArgAspThrAspProAspThrPheLeuLysHisIleLys	483	
Db	2188	CAATATGATGTGGAAAGACCGCTGGCTGCCATATAACAACTTTTGACCGTCCCATTTGAA	2247	
QY	484	Lys-----ValIleGluLysGlyTyrArgGluLysGlnAlaIle	497	
Db	2248	ACGAGCAGTTCGCGCCGCTATCTTATTGAATTTAAACATCGCTTAAAGGACAGCTCAT	2307	
QY	498	GluTyr-----SerGlyLeuThrGluThrGln	506	
Db	2308	AAGCAGCATCTTACACCAATAAAGGCCAGTACCATATATGCCGATATTACAGCGTGA	2367	
QY	507	LeuAlaGlnAlaThrGlnLeuAlaIleTyrTyrPheThrAspSerAlaGlnLeuAspLys	526	
Db	2368	TTTGAGCGCATCCGTTTCGGTGCACA-----GACGAGAGAAAGCTCGTTTTC	2412	
QY	527	AspLysLeuLysAspTyrHisGlyPheGlyAsp-----MetAspSerThr	542	
Db	2413	AAAGGAGGCACAAACAAACGAGGTTATTCGATTGGACATCAATGTCAACGCGACCGAG	2472	
QY	543	LeuAlaValAlaTyrIleLeuValGluTyrIleAsnSerAsnProProGlnLeuThr	562	
Db	2473	TCGGTGTGGAAAGATGTAAAGTACCGATCTCCGATACCAAT-----CAATTTTAA	2526	
QY	563	AspLeuAspPhePhe-----	567	
Db	2527	GCTGAGATTCCTTTTAAAGTTATTCAGGCTAAATATGATGAAAAAGTGCAGTCAAAAG	2586	
QY	567	-----	567	
Db	2587	AGCAGCGGAATCTTGTCCCGGATGATGTTCAGCTTAAGAAAGCGAGACTATACACTG	2646	
QY	568	--IleProAsnAsnAsn-----	572	
Db	2647	GATATCAAGACCGACAATGCAACCGGCGACAAATCATCTTGTCTGAATTTACAGCGAT	2706	
QY	573	-----LysTyrGlnSerLeuIle-----Gly	579	
Db	2707	TACAAAAAATATGACCGCGCTATGTATTAATCAATATCAATATGATTCATATTTCCGCG	2766	
QY	580	ThrGlnTrpHisProGluAspLeuValAspIleIle-----Arg	592	
Db	2767	ACGAGCGCCCATGTTTACACAAAGATGTCTGATTTCCGGAACAGATGTCCAGGAACAGAC	2826	
QY	593	MetGluAspLysLysGluValIleProValThrHis-----	604	
Db	2827	CAGGAAACACAGAGCTCGCTTTGTGGCCGTTTCAAGCGCGCGGTACGGTCAAGG	2886	
QY	605	-----AsnLeuThrLeuArgLysThrValThrGlyLeuAlaGlyAspArgThrLys	621	
Db	2887	GAAAGAGGAACCTCGACATCTTTAAA-----ACGGGAGAAAGACGGGAGCGCCGCTTCC	2940	
QY	622	AspPheHisPheGluIleGluLeuLysAsnLysGlnGluLeuLeuSerGlnThrVal	641	
Db	2941	GGAGCAGATTTTTCATTTCCGACAAAGATATATAGCAG-----CTTCCTCGGACACGA	2994	
QY	642	LysThrAspLysThrAsnLeuGluPheLysAspGlyLysAlaThrIle-----AsnLeuLys	660	



QY 611 -----ThValThrgLLeuAlaGlyAspArgThrLysAspPheHisPheGluIleG1 628  
Db 10294 TGACTTACAGTATTATAAAAAAGCGATATACAGC-----CC 10332  
QY 628 uLeuLysAsnAsnLysGlnGlnLeuLeuSerGlnThrValLysThrAspLysThrAsnLe 648  
Db 10333 ACTTAAAGACGCAATTCCTTACAGCA-----CCAGATACGATAT 10377  
QY 648 uGluPhe-----LysAspGlyLysAlaThr-----IleAsnLeuLysHisG1 662  
Db 10378 TGAATTACCAAAAGATGGCAAGAAAGCAGTACTTTGTTTGAACCTTAAACCCAGG 10437  
QY 662 yGlu---SerLeuThrLeuGlnGlnLysLeuProGluGlyTyrSerTyrLeuValLysGluTh 681  
Db 10438 GAATATGTTCTTACAGAAACCTTACGCGCAAGGATATCAGGGCTTAAAGAACCAAT 10497  
QY 681 rAsp-----SerGluGlyTyrLysValLysValAsnSerGlnGlnValAlaAsnAl 698  
Db 10498 CGAATTATATATTCGTGAAGATGGTTCAGTCACGATGATGGGAAAGATGACGATGT 10557  
QY 698 aThrValSer-----LysThrGlyIleThrSerAspGluThrIleuAlaPheGluAs 715  
Db 10558 TTTATTTCTGGAAGAAAGATTAATCAATTACTTTAGACGTTAG-----AACCA 10608  
QY 715 nasuLysGluProValValProThrGlyValAspGlnLysLysLeuGlnGlyTyrLeuAlaLe 735  
Db 10609 AGCAAGGTTCTTACTGAACTGTCGATAGAGGCGTTCGCTTACTTCTGATAGC 10668  
QY 735 uIle-----ValIleAlaGlyIleSerLeuGlyIle 745  
Db 10669 GATTAGTACATTCGTATAGCGGGTGTATTATCTTAT 10708

RESULT 2  
US-09-070-927A-242  
Sequence 242, Application US/09070927A  
Patent No. US20020120116A1  
GENERAL INFORMATION:  
APPLICANT: Charles A. Kunsch  
Patrick J. Dillon  
Steven Barash  
TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides  
NUMBER OF SEQUENCES: 982  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/070,927A  
FILING DATE: 04-May-2000  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/046,655  
FILING DATE: 1997-05-16  
APPLICATION NUMBER: 60/044,031  
FILING DATE: 1997-05-06  
APPLICATION NUMBER: 60/066,009  
FILING DATE: 1997-11-14  
ATTORNEY/AGENT INFORMATION:  
NAME: Kenley K. Hoover  
REGISTRATION NUMBER: 40,302  
REFERENCE/DOCKET NUMBER: PB369  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 242:

SEQUENCE CHARACTERISTICS:  
LENGTH: 12445 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 242:  
US-09-070-927A-242

Alignment Scores:  
Pred. No.: 0.000118 Length: 12445  
Score: 161.00 Matches: 159  
Percent Similarity: 34.83% Conservative: 104  
Best Local Similarity: 21.06% Mismatches: 326  
Query Match: 4.08% Indels: 166  
Gaps: 40

US-09-494-297-2 (1-757) x US-09-070-927A-242 (1-12445)

QY 39 AlaLeuValThrSerMetValGlyAlaLysThrValPheGlyLeuValGluSer----- 56  
Db 9634 TCATTAAGTACACCTGATATGTCCTTAATAAGCATCAATTATGATCCGATCAATAT 9693  
QY 57 ---SerThrProAsnAlaIleAsnProAspSerSerSerGluTyrArgTyrGlyTyr 75  
Db 9694 ATTGAACCAATTAAGTGTTAATCCT---TTGAATGCTGAAGTCTTGCGGTAAATAT 9750  
QY 76 GluSerTyrValArgGlyHisProTyrTyrLysGlnPheArgValAlaHisAspLeuArg 95  
Db 9751 GATCAA-----AATGTCCTATTCATCAAGA 9777  
QY 96 -----ValAsnLeuGlnGlySerArgSerTyrGlnValTyrCysPheAsnLeuLysLys 113  
Db 9778 ACAACTGCTCAGTATATGGAAGCAAGAAACCGATTCAAAATTGAAATTAAGTA 9837  
QY 114 AlaPhePro-----LeuGlySerAspSerSerValLysTyrTyrLysLys 129  
Db 9838 AAGCATCCTAATTATCTTCAATTACAGCTCAAAAGAAATTAATTATTTATACAAAG--- 9894  
QY 130 HisAspGlyIleSerThrLysPheGluSprLysIleMetSerProArgIleThrGlySpr 149  
Db 9895 -----TTAGGACG-----GATTATACAGTACGCCACGTCAGATGTCGA 9936  
QY 150 GluLeuAsnGlnLysLeuArgAlaValMetLysGlnLysProGlnAsnAlaAsnGly 169  
Db 9937 GTTATTAAGTACACGACCCCAATAACAGAAATCCAAATTCATGTTTAAATAT 9996  
QY 170 IleMetGlyLysLeuGlu-----ProLeuAsnAlaIleArgValThrGln 184  
Db 9997 GTGCCAGATAGTTCGCCAAAGATTAAGTATCCAGTCAGATACGATACGATTAACATG 10056  
QY 185 GluAlaValIlePyrTyrSerAspAsnAlaProIleSerAsnProAspGluSerPheLys 204  
Db 10057 AGTCGTGAAGGTTTAACCTCAGTATGACAGATCACTACT-----AATAGTAG 10107  
QY 205 ArgGluSerGlnSerAsnLeuValSerThrSerGlnLeuSerLeuMetArgIleAlaLeu 224  
Db 10108 CGTGGTTTGAACGACACTTCAAGTAGTAAATATCAATTCCTTGTAATGACAGAAAT 10167  
QY 225 LysGlnLeuIleAspProAsnLeuAlaThrLysMetProLysGlnValProAspAspPhe 244  
Db 10168 GATTCCTTTGACTCAGTACAGGTCGCTCAAAATTCACAGTGGCGCC-----GATGTT 10221  
QY 245 GlnLeuSerIlePheGluSerGlnAspLysGlyAspLysTyrAsnLysGlyTyrGlnAsn 264  
Db 10222 CTTTTCGATTTATGATGATTTCAAC-----GATCAGTAGATTCATTTATTCACAA 10275  
QY 265 LeuLeuSerGlyGlyLeuValProThrLysProThrProThrProGlyAspProPhePro 284  
Db 10276 TACTGGACCGCGGTCAATACTTGTGATTAACCAATGAGCCAAACAGCCCTGGATATCA 10335  
QY 285 -----ProAsnGlnProGlnThrThrSerValleuIle-----Arg 296  
Db 10336 AGCATTACTTTGACGAAATATACCAATAGTTACAGCTTGTGATTTTGAATAACCAACAA 10395

```

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB369
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 15614 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-070-927A-45
US-09-494-297-2 (1-757) x US-09-070-927A-45 (1-15614)

Alignment Scores:
Pred. No.: 5, 91e-08 Length: 15614
Score: 196.00 Matches: 165
Percent Similarity: 35.57% Conservative: 89
Best Local Similarity: 23.11% Mismatches: 245
Query Match: 4.97% Indels: 216
Gaps: 41

DB:
10
9523 TACACAAATCAAGGACAAAGCTTTCAAT-----TATCAAAACAACCCGTAATATAGCA--- 9573

```

```

271 ValProThrLysProProThrProGlyAspProPromeProProAsnGlnProGlnThr 290
9574 GTTCTCGGTGTACAGTCAAGAAAAATCGAGATACTACTGGAAAAACAGCAAGCTTC 9633
291 ThrSerVal-----LeuIleArgLysTyrAlaIleGlyAspTyrSerLysLeu 307
9634 AACCATTTGATTTAAAGATCAAAATTTCTCCAGGTAG-----AAAACCTTA 9687
308 GluGlyAlaThrLeuGlnLeuThrGlyAspAsnValAsnSerPheGlnAlaArgValPhe 327
9688 GTGGGAGCCGCTCTTGAATTGAGTCAAAAATGTT-----CAAAACAACTTAAGTG 9738
328 SerSerAsnAsp-----IleGlyGluArgIleGluLeuSerAspGly-----Thr 342
9739 GACAAATAAAGATGGTACTATTCCTCCCAAAAAGATGGCGCTACAAAAAGGGGAACGC 9798
343 TyrThrLeuThrGluLeuAsnSerProAlaGlyTyrSerIleAlaGluProIleThrPhe 362
9799 TATACATTAAGTAAAGTAAAGCAAGCCTGCAGACATGAGTTAGCAAGAAAGCACTTGC 9858
363 LysValGluAla-----GlyLysValTyrThrIleLeuAspGlyLysGlnIleGlu 379
9859 CAAATTGAGGTGAGTGAAGCAAGCAAGTA-----AGCATCGATGACAAAGAGTACC 9912
380 AsnProAsnLysGluIleValGluProTyrSerValGluAlaTyrAsnAspPheGlu 399
9913 ACCCAAAATCAAGTAAAT-----CCATTGGAAATTTGA-----ATAAATTTCTTCT 9960
400 PheSerVal-----LeuThrThrGlnAsnTyrAlaLysPheTyrTyrAlaLys 415
9961 TTGCAATCAAGATTTGAATAATACCAATGCAAAAT-----GGCAAA 10002
416 AsnLysAsnGlySerSerGlnValValTyrCysPheAsnAlaAspLeuSerProPr 435
10003 CAAGTCACTTACCAAGGAGGACTTTGGCTTCCCAAGAA----- 10042
435 AspSerGluAspGlyGlyLysThrMetThrProAspPheThrThrGlyGluValLysTyr 455
10043 -----AAAATGCTGCAGAGAAGTTACCAAACTGTGCAAACTGAAA 10083
455 rThrHisIleAlaGlyArgAspLeuPheLysTyrThrValLysProArgAspThrAspPr 475
10084 AACGATACTACAGATGAGTATGATTT----- 10111
475 AspThrPheLeuLysHisIleLysValIleGluLysGly-----TyrArgGluLysG 494
10112 -----AAAATTAGTGAACCTGGTGAATCGA----- 10138
494 yGlnAlaIleGluTyrSerGlyLeuThrGlnLeuArgAlaAlaThrGlnLeuAl 514
10139 -----ATGGTGGAAATCAACAG-----CCATTAGGCTACGACACTTCTGTGG 10182
514 aIleTyrTyrPheThrAspSerAlaGluLeuAspLysAspLysLeuLysAspTyrHisG 534
10183 AAATTTAGATTACT-----GTTGATAAA----- 10207
534 yPheGlyAspMetAsnAspSerThrLeuAlaValAlaLysIleLeuValGluTyrAlaG 554
10208 -TATGGGAAA-----ATTCACTATTCACAG 10230
554 n-----AspSerAsnProGlnLeuThrAspLeuAspPhePheIleProAsnAs 571
10231 CAAAAATATTGAAGAAATATCGCGCAATAGACA----- 10264
571 nAsnLysTyrGlnSerLeuIleGlyThrGlnThrHisProGluAspLeuValAspIleI 591
10264 ----- 10264
591 eArgMetGluAspLysGluValIleProValThrHisAsnLeuThrLeuArgLys--- 610
10265 -----CTGACACATCAAAATTAATTTGAACCTTT 10293

```



GenCore version 5.1.6  
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## OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 19, 2003, 17:28:10 ; Search time 459 Seconds

(without alignments)  
3690.895 Million cell updates/sec

Title: US-09-494-297-2

Perfect score: 3945  
Sequence: 1 MKTRFPKRLNTLNTQRYLS.....IAGISLIGIMGHTIRKRD 757

## Scoring table:

BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 1504479 seqs, 1118970152 residues

Total number of hits satisfying chosen parameters: 3008958

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Command line parameters:

```
-MODEL=frame+p2n model -DEV=xlp  
-Q=/cgn2_1/USPFO_US09494297/runat_13082003.122948.28206/app.query.fasta_1.903  
-DB=Published.Applications_NA -OFMT=fastap -SUFFIX=trpb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=Dlosum62  
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=pcr -THR_MAX=100  
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US09494297 @CGN1.1.252 @runat_13082003.122948.28206  
-NCPU=6 -ICPU=3 -NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSEBLOCK=100  
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

## Database :

```
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*  
2: /cgn2_6/ptodata/2/pubpna/PCCT_NEW_PUB.seq:*  
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*  
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*  
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*  
6: /cgn2_6/ptodata/2/pubpna/PCCT_PUBCOMB.seq:*  
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*  
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*  
9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*  
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*  
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*  
12: /cgn2_6/ptodata/2/pubpna/US09A_NEW_PUB.seq:*  
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*  
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*  
15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*  
16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*  
17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
```

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	196	5.0	15614	10 US-09-070-927A-45 Sequence 45, Appl

2	161	4.1	12445	10 US-09-070-927A-242 Sequence 242, App
3	156	4.0	4557	10 US-09-974-300-2632 Sequence 2632, Ap
4	152	3.9	5547	14 US-10-242-056-48 Sequence 48, Appl
5	152	3.9	7551	9 US-09-817-514A-1 Sequence 1, Appl1
6	152	3.9	7551	14 US-10-242-056-46 Sequence 46, Appl
7	149	3.8	27360	10 US-09-070-927A-164 Sequence 164, App
8	148	3.8	3827	10 US-09-870-759-44 Sequence 44, Appl
9	147	3.7	4047	9 US-09-815-242-4843 Sequence 4843, Ap
10	147	3.7	4050	9 US-09-815-242-9039 Sequence 9039, Ap
11	146.5	3.7	2522	9 US-09-842-552-98 Sequence 98, Appl
12	144.5	3.7	7035	9 US-09-815-242-8615 Sequence 8615, Ap
13	139.5	3.5	3504	9 US-09-815-242-7425 Sequence 7425, Ap
14	139	3.5	7101	14 US-10-011-366-9 Sequence 9, Appl1
15	139	3.5	19031	10 US-09-070-927A-167 Sequence 167, App
16	137.5	3.5	20072	10 US-09-070-927A-89 Sequence 89, Appl
17	137	3.5	9509	10 US-09-070-927A-364 Sequence 364, App
18	136.5	3.5	2523	9 US-09-815-242-4724 Sequence 4724, Ap
19	136.5	3.5	2526	9 US-09-815-242-8653 Sequence 8653, Ap
20	136.5	3.5	4358	8 US-08-781-986A-454 Sequence 454, App
21	136.5	3.5	6806	8 US-08-781-986A-472 Sequence 472, App
22	136.5	3.5	14756	14 US-10-160-758-5 Sequence 5, Appl1
23	136.5	3.5	14756	14 US-10-060-026-134 Sequence 134, App
24	135.5	3.4	2661	11 US-09-769-787-338 Sequence 338, App
25	135	3.4	3687	10 US-09-117-447-1 Sequence 1, Appl1
26	134.5	3.4	14934	14 US-10-084-817-227 Sequence 227, App
27	133.5	3.4	2412	11 US-09-919-039-144 Sequence 144, App
28	133.5	3.4	2616	10 US-09-858-525A-1 Sequence 1, Appl1
29	133.5	3.4	20561	10 US-09-070-927A-292 Sequence 292, App
30	132.5	3.4	2458	11 US-09-919-039-145 Sequence 145, App
31	132.5	3.4	2636	13 US-10-002-600-95 Sequence 95, Appl
32	131.5	3.3	2766	10 US-09-117-447-5 Sequence 527, App
33	131.5	3.3	7107	10 US-09-070-927A-527 Sequence 27, Appl
34	131	3.3	6360	12 US-09-769-744A-27 Sequence 7, Appl1
35	130.5	3.3	14536	14 US-10-160-758-7 Sequence 39, App
36	129.5	3.3	1998	11 US-09-769-787-339 Sequence 9, Appl1
37	129.5	3.3	2520	10 US-09-858-525A-9 Sequence 266, App
38	129.5	3.3	4702	8 US-08-781-986A-268 Sequence 264, App
39	129.5	3.3	5171	8 US-08-781-986A-264 Sequence 62, Appl
40	129.5	3.3	11560	14 US-10-177-293-62 Sequence 168, App
41	128.5	3.3	7963	8 US-08-781-986A-168 Sequence 460, App
42	128	3.2	4226	14 US-10-037-270-480 Sequence 1, Appl1
43	128	3.2	4319	11 US-09-839-996-1 Sequence 1, Appl1
44	128	3.2	4319	14 US-10-080-505-1 Sequence 3, Appl1
45	128	3.2	4896	9 US-09-740-274-3

## ALIGNMENTS

## RESULT 1

US-09-070-927A-45  
; Sequence 45, Application US/09070927A

Patent No. US20020120116A1  
GENERAL INFORMATION:

APPLICANT: Charles A. Kunsch

Steven Barash  
Patrick J. Dillon

TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides

NUMBER OF SEQUENCES: 982

CORRESPONDENCE ADDRESS:

ADDRESS: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/070,927A

FILING DATE: 04-May-2000